

SEQUENCE LISTING

<110> MBARI

DeLong, Edward

Beja, Oded

<120> Light-driven energy generation using proteorhodopsin

<130> MBA-101

<150> 60/201,602

<151> 2000-05-03

<160> 65

<170> PatentIn version 3.0

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<211> 105184

<212> DNA

<213> Naturally occurring gamma proteobacterium

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<221> CDS (complement)

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gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg	240
Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met	
65 70 75 80	
aga ggg gta tgg att gaa act ggt gat tcg cca act gta ttt aga tac	288
Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr	
85 90 95	
att gat tgg tta cta aca gtt cct cta tta ata tgt gaa ttc tac tta	336
Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu	
100 105 110	
att ctt gct gct gca act aat gtt gct gga tca tta ttt aag aaa tta	384
Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu	
115 120 125	
cta gtt ggt tct ctt gtt atg ctt gtg ttt ggt tac atg ggt gaa gca	432
Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala	
130 135 140	
gga atc atg gct gca tgg cct gca ttc att att ggg tgt tta gct tgg	480
Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp	
145 150 155 160	
gta tac atg att tat gaa tta tgg gct gga gaa gga aaa tct gca tgt	528
Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys	
165 170 175	
aat act gca agt cct gct gtg caa tca gct tac aac aca atg atg tat	576
Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr	
180 185 190	
att atc atc ttt ggt tgg gcg att tat cct gta ggt tat ttc aca ggt	624
Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly	
195 200 205	
tac ctg atg ggt gac ggt gga tca gct ctt aac tta aac ctt atc tat	672
Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr	
210 215 220	

Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu
 115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
 130 135 140

Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp
 145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys
 165 170 175

Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr
 180 185 190

Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
 195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
 210 215 220

Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
 225 230 235 240

Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 6

<211> 747

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(747)

<223> Native proteorhodopsin DNA sequence from BAC clone 31A08

<300>

<301> Beja,O., Aravind,L., Koonin,E.V., Suzuki,M.T., Hadd,A.,
Nguyen,L.P., Jovanovich,S.B., Gates,C.M., Feldman,R.A., Spudich,J.L.,
Spudich,E.N. and DeLong,E.F.

<302> Bacterial rhodopsin: evidence for a new type of phototrophy in
the sea

<303> Science

<304> 289

<305> 5486

<306> 1902-1906

<307> 2000-09-15

<309> _____

<313> (1)..(747)

<400> 6

atg aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca ttt 48
Met Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr Phe
1 5 10 15

gct gca ggt ggt ggt gac ctt gat gct agt gat tac act ggt gtt tct 96
Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val Ser
20 25 30

ttt tgg tta gtt act gct gct tta tta gca tct act gta ttt ttc ttt 144
Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe Phe
35 40 45

500 450 400 350 300 250 200 150 100 50

gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act gta Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr Val 50 55 60	192
tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg aga Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met Arg 65 70 75 80	240
ggg gta tgg att gaa act ggt gat tcg cca act gta ttt aga tac att Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr Ile 85 90 95	288
gat tgg tta cta aca gtt cct cta tta ata tgt gaa ttc tac tta att Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu Ile 100 105 110	336
ctt gct gct gca act aat gtt gct gga tca tta ttt aag aaa tta cta Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu Leu 115 120 125	384
gtt ggt tct ctt gtt atg ctt gtg ttt ggt tac atg ggt gaa gca gga Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala Gly 130 135 140	432
atc atg gct gca tgg cct gca ttc att att ggg tgt tta gct tgg gta Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp Val 145 150 155 160	480
tac atg att tat gaa tta tgg gct gga gaa gga aaa tct gca tgt aat Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys Asn 165 170 175	528
act gca agt cct gct gtg caa tca gct tac aac aca atg atg tat att Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr Ile 180 185 190	576
atc atc ttt ggt tgg gcg att tat cct gta ggt tat ttc aca ggt tac Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly Tyr 195 200 205	624
ctg atg ggt gac ggt gga tca gct ctt aac tta aac ctt atc tat aac Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr Asn 210 215 220	672
ctt gct gac ttt gtt aac aag att cta ttt ggt tta att ata tgg aat Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp Asn 225 230 235 240	720

gtt gct gtt aaa gaa tct tct aat gct
 Val Ala Val Lys Glu Ser Ser Asn Ala
 245

<210> 7

<211> 249

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 7

Met Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr Phe
 1 5 10 15

Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val Ser
 20 25 30

Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe Phe
 35 40 45

Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr Val
 50 55 60

Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met Arg
 65 70 75 80

Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr Ile
 85 90 95

Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu Ile
 100 105 110

Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu Leu
 115 120 125

Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala Gly
 130 135 140

Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp Val
 145 150 155 160

Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys Asn
 165 170 175

Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr Ile
 180 185 190

Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly Tyr
 195 200 205

Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr Asn
 210 215 220

Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp Asn
 225 230 235 240

Val Ala Val Lys Glu Ser Ser Asn Ala
 245

<210> 8

<211> 750

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(750)

<223> proteorhodopsin variant from clone EBAC40

<400> 8

atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca	48
Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr	
1 5 10 15	

ttt gct gca ggt ggt ggt gac ctt gat gct agt gat tac act ggt gtt	96
Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val	
20 25 30	

tct ttt tgg tta gtt act gct gct cta tta gca tct act gta ttt ttc	144
Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe	
35 40 45	

ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act	192
Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr	
50 55 60	

gta tcg ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg	240
Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met	
65 70 75 80	

aga ggg gta tgg att gag act ggt gat tcg cca act gta ttt aga tac	288
Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr	
85 90 95	

att gat tgg tta cta aca gtt cct cta ttg ata tgt gaa ttc tac tta	336
Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu	
100 105 110	

att ctt gct gct gca aca aat gtt gct gct ggc ctg ttt aag aaa tta	384
Ile Leu Ala Ala Ala Thr Asn Val Ala Ala Gly Leu Phe Lys Lys Leu	
115 120 125	

ttg gtt ggt tct ctt gtt atg ctt gtg ttt ggt tac atg ggt gag gca	432
Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala	
130 135 140	

gga att atg aac gct tgg ggt gca ttc gtt att ggg tgt tta gct tgg	480
Gly Ile Met Asn Ala Trp Gly Ala Phe Val Ile Gly Cys Leu Ala Trp	
145 150 155 160	

gta tac atg att tat gaa cta tgg gct gga gaa ggc aag gct gca tgt	528
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Val	Tyr	Met	Ile	Tyr	Glu	Leu	Trp	Ala	Gly	Glu	Gly	Lys	Ala	Ala	Cys		
				165					170					175			
aat	act	gca	agt	cct	gct	gtg	caa	tca	gct	tac	aac	aca	atg	atg	tat		576
Asn	Thr	Ala	Ser	Pro	Ala	Val	Gln	Ser	Ala	Tyr	Asn	Thr	Met	Met	Tyr		
			180					185					190				
ata	atc	atc	ttt	ggg	tgg	gca	att	tat	cct	gta	ggg	tat	ttc	aca	ggg		624
Ile	Ile	Ile	Phe	Gly	Trp	Ala	Ile	Tyr	Pro	Val	Gly	Tyr	Phe	Thr	Gly		
			195				200					205					
tac	cta	atg	ggg	gac	ggg	gga	tca	gct	ctt	aac	tta	aac	ctt	atc	tat		672
Tyr	Leu	Met	Gly	Asp	Gly	Gly	Ser	Ala	Leu	Asn	Leu	Asn	Leu	Ile	Tyr		
	210					215					220						
gac	ctt	gct	gac	ttt	gtt	aac	aag	att	cta	ttt	ggg	tta	att	ata	tgg		720
Asp	Leu	Ala	Asp	Phe	Val	Asn	Lys	Ile	Leu	Phe	Gly	Leu	Ile	Ile	Trp		
225					230					235					240		
aat	gtt	gct	gtt	aaa	gaa	tct	tct	aat	gct								750
Asn	Val	Ala	Val	Lys	Glu	Ser	Ser	Asn	Ala								
				245					250								
<210>	9																
<211>	250																
<212>	PRT																
<213>	Naturally occurring gamma proteobacterium																
<400>	9																
Met	Gly	Lys	Leu	Leu	Leu	Ile	Leu	Gly	Ser	Val	Ile	Ala	Leu	Pro	Thr		
1				5					10					15			
Phe	Ala	Ala	Gly	Gly	Gly	Asp	Leu	Asp	Ala	Ser	Asp	Tyr	Thr	Gly	Val		
			20					25					30				
Ser	Phe	Trp	Leu	Val	Thr	Ala	Ala	Leu	Leu	Ala	Ser	Thr	Val	Phe	Phe		
		35					40					45					

101050-ET54360

Asn Val Ala Val Lys Glu Ser Ser Asn Ala
245 250

<210> 10

<211> 750

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(750)

<223> proteorhodopsin variant from clone EBAC41

<400> 10
atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca 48
Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
1 5 10 15

ttt gct gca ggt ggt ggt gac ctt gat gct agt gat tac act ggt gtt 96
Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
20 25 30

tct ttt tgg tta gct act gct gct tta tta gca tct act gta ttt ttc 144
Ser Phe Trp Leu Ala Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
35 40 45

ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act 192
Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50 55 60

gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg 240
Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
65 70 75 80

aga ggg gta tgg att gaa act ggt gat tcg cca act gta ttt aga tac 288
Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
85 90 95

att gat tgg tta cta aca gtt cct cta tta ata tgt gaa ttc tac tta	336
Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu	
100 105 110	
att ctt gct gct gct act aat gtt gct gga tca tta ttt aag aaa tta	384
Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu	
115 120 125	
cta gtt ggt tct ctt gtt atg ctt gtg ttt ggt tac atg ggt gaa gca	432
Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala	
130 135 140	
gga atc atg gct gca tgg cct gca ttc att att ggg tgt tta gct tgg	480
Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp	
145 150 155 160	
gta tac atg att tat gaa cta tgg gct gga gaa gga aaa tct gca tgt	528
Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys	
165 170 175	
aat act gca agt cct gct gtg caa tca gct tac aac aca atg atg tat	576
Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr	
180 185 190	
att atc atc ttt ggt tgg gcg att tat cct gta ggt tat ttc aca ggt	624
Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly	
195 200 205	
tac ctg atg ggt gac ggt gga tca gct ctt aac tta aac ctt atc tat	672
Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr	
210 215 220	
aac ctt gct gat ttt gtt aac aag att cta ttt ggt tta att ata tgg	720
Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp	
225 230 235 240	
aat gtt gct gtt aaa gaa tct tct aat gct	750
Asn Val Ala Val Lys Glu Ser Ser Asn Ala	
245 250	

<210> 11

<211> 250

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 11

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
1 5 10 15

Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
20 25 30

Ser Phe Trp Leu Ala Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
35 40 45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
100 105 110

Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu
115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
130 135 140

Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp
145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys
165 170 175

Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr
180 185 190

Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
210 215 220

Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
225 230 235 240

Asn Val Ala Val Lys Glu Ser Ser Asn Ala
245 250

<210> 12

<211> 750

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(750)

<223> Proteorhodopsin variant from clone EBAC64

<400> 12

atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca	48
Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr	
1 5 10 15	

ttt gct gca ggt ggc ggt gac ctt gat gct agt gat tac act ggt gtt	96
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Phe	Ala	Ala	Gly	Gly	Gly	Asp	Leu	Asp	Ala	Ser	Asp	Tyr	Thr	Gly	Val	
			20					25					30			
tct	ttt	tgg	tta	gtt	aca	gct	gct	cta	tta	gca	tct	act	gta	ttt	ttc	144
Ser	Phe	Trp	Leu	Val	Thr	Ala	Ala	Leu	Leu	Ala	Ser	Thr	Val	Phe	Phe	
		35					40					45				
ttt	gtt	gaa	aga	gat	aga	gtt	tct	gca	aaa	tgg	aaa	aca	tca	tta	act	192
Phe	Val	Glu	Arg	Asp	Arg	Val	Ser	Ala	Lys	Trp	Lys	Thr	Ser	Leu	Thr	
	50					55					60					
gta	tct	ggg	ctt	gtt	act	ggg	att	gct	ttc	tgg	cat	tac	atg	tac	atg	240
Val	Ser	Gly	Leu	Val	Thr	Gly	Ile	Ala	Phe	Trp	His	Tyr	Met	Tyr	Met	
65					70					75					80	
aga	gga	gta	tgg	att	gaa	act	ggg	gat	tcg	cct	act	gta	ttt	aga	tac	288
Arg	Gly	Val	Trp	Ile	Glu	Thr	Gly	Asp	Ser	Pro	Thr	Val	Phe	Arg	Tyr	
				85					90					95		
att	gat	tgg	tta	cta	aca	gtt	cct	tta	tta	ata	tgt	gaa	ttc	tac	tta	336
Ile	Asp	Trp	Leu	Leu	Thr	Val	Pro	Leu	Leu	Ile	Cys	Glu	Phe	Tyr	Leu	
			100					105					110			
att	ctt	gct	gct	gca	act	aat	gtt	gcc	ggc	tca	tta	ttt	aag	aaa	ctt	384
Ile	Leu	Ala	Ala	Ala	Thr	Asn	Val	Ala	Gly	Ser	Leu	Phe	Lys	Lys	Leu	
		115					120					125				
cta	gtt	ggg	tct	ctt	gtt	atg	ctt	gtg	ttt	ggg	tac	atg	ggg	gaa	gca	432
Leu	Val	Gly	Ser	Leu	Val	Met	Leu	Val	Phe	Gly	Tyr	Met	Gly	Glu	Ala	
	130					135					140					
gga	att	atg	gca	gct	tgg	cct	gca	ttc	att	att	ggg	tgt	tta	gct	tgg	480
Gly	Ile	Met	Ala	Ala	Trp	Pro	Ala	Phe	Ile	Ile	Gly	Cys	Leu	Ala	Trp	
145					150					155					160	
gta	tac	atg	att	tat	gaa	cta	tat	gct	gga	gaa	gga	aaa	tct	gca	tgt	528
Val	Tyr	Met	Ile	Tyr	Glu	Leu	Tyr	Ala	Gly	Glu	Gly	Lys	Ser	Ala	Cys	
				165					170					175		
aat	act	gca	agt	cct	tcg	gtt	caa	tca	gct	tac	aac	aca	atg	atg	gct	576
Asn	Thr	Ala	Ser	Pro	Ser	Val	Gln	Ser	Ala	Tyr	Asn	Thr	Met	Met	Ala	
			180					185					190			
atc	ata	gtc	ttc	ggg	tgg	gca	att	tat	cct	ata	ggg	tat	ttc	aca	ggg	624
Ile	Ile	Val	Phe	Gly	Trp	Ala	Ile	Tyr	Pro	Ile	Gly	Tyr	Phe	Thr	Gly	
		195					200					205				
tac	cta	atg	ggg	gac	ggg	gga	tca	gct	ctt	aac	tta	aac	ctt	att	tat	672

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
 210 215 220

aac ctt gct gac ttt gtt aac aag att cta ttt ggt tta att ata tgg 720
 Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
 225 230 235 240

aat gtt gct gtt aaa gaa tct tct aat gct 750
 Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 13

<211> 250

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 13

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
 1 5 10 15

Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30

Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
 65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
 85 90 95

<220>

<221> CDS

<222> (1)..(750)

<223> Proteorhodopsin variant from pcr clone HOT01m: GenBank# AF349978

<400> 14

atg	ggt	aaa	tta	tta	ctg	ata	tta	ggt	agt	ggt	att	gca	ctt	cct	aca	48
Met	Gly	Lys	Leu	Leu	Leu	Ile	Leu	Gly	Ser	Val	Ile	Ala	Leu	Pro	Thr	
1			5					10					15			

ttt	gct	gca	ggt	ggt	ggt	gac	ctt	gat	gct	agt	gat	tac	act	ggt	ggt	96
Phe	Ala	Ala	Gly	Gly	Gly	Asp	Leu	Asp	Ala	Ser	Asp	Tyr	Thr	Gly	Val	
			20					25					30			

tct	ttt	tgg	tta	ggt	act	gct	gct	cta	tta	gca	tct	act	gta	ttt	ttc	144
Ser	Phe	Trp	Leu	Val	Thr	Ala	Ala	Leu	Leu	Ala	Ser	Thr	Val	Phe	Phe	
		35					40					45				

ttt	ggt	gaa	aga	gat	aga	ggt	tct	gca	aaa	tgg	aaa	aca	tca	tta	act	192
Phe	Val	Glu	Arg	Asp	Arg	Val	Ser	Ala	Lys	Trp	Lys	Thr	Ser	Leu	Thr	
	50					55					60					

gta	tcg	ggt	ctt	ggt	act	ggt	att	gct	ttc	tgg	cat	tac	atg	tac	atg	240
Val	Ser	Gly	Leu	Val	Thr	Gly	Ile	Ala	Phe	Trp	His	Tyr	Met	Tyr	Met	
65					70					75					80	

aga	ggg	gta	tgg	att	gag	acc	ggt	gat	tcg	cca	act	gta	ttt	aga	tac	288
Arg	Gly	Val	Trp	Ile	Glu	Thr	Gly	Asp	Ser	Pro	Thr	Val	Phe	Arg	Tyr	
				85					90					95		

att	gat	tgg	tta	cta	aca	ggt	cct	cta	ttg	ata	tgt	gaa	ttc	tac	tta	336
Ile	Asp	Trp	Leu	Leu	Thr	Val	Pro	Leu	Leu	Ile	Cys	Glu	Phe	Tyr	Leu	
			100					105					110			

att	ctt	gct	gct	gca	aca	aat	ggt	gct	gct	ggc	ctg	ttt	aag	aaa	tta	384
Ile	Leu	Ala	Ala	Ala	Thr	Asn	Val	Ala	Ala	Gly	Leu	Phe	Lys	Lys	Leu	
		115					120					125				

ttg	ggt	ggt	tct	ctt	ggt	atg	ctt	gtg	ttt	ggt	tac	atg	ggt	gag	gca	432
Leu	Val	Gly	Ser	Leu	Val	Met	Leu	Val	Phe	Gly	Tyr	Met	Gly	Glu	Ala	

130	135	140	
gga att atg aac gct tgg ggt gca ttc gtt att ggg tgt tta gct tgg			480
Gly Ile Met Asn Ala Trp Gly Ala Phe Val Ile Gly Cys Leu Ala Trp			
145	150	155	160
gta tac atg att tat gaa cta tgg gct gga gaa ggc aag gct gca tgt			528
Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ala Ala Cys			
	165	170	175
aat act gca agt cct gct gtg caa tca gct tac aac aca atg atg tat			576
Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr			
	180	185	190
ata atc atc ttt ggt tgg gca att tat cct gta ggt tat ttc aca ggt			624
Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly			
	195	200	205
tac cta atg ggt gac ggt gga tca gct ctt aac tta aac ctt atc tat			672
Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr			
	210	215	220
aac ctt gct gac ttt gtt aac aag att cta ttt ggt tta att ata tgg			720
Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp			
	225	230	235
aat gtt gct gtt aaa gaa tct tct aat gct			750
Asn Val Ala Val Lys Glu Ser Ser Asn Ala			
	245	250	

<210> 15

<211> 250

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 15

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
1 5 10 15

Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val

20

25

30

Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
35 40 45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
100 105 110

Ile Leu Ala Ala Ala Thr Asn Val Ala Ala Gly Leu Phe Lys Lys Leu
115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
130 135 140

Gly Ile Met Asn Ala Trp Gly Ala Phe Val Ile Gly Cys Leu Ala Trp
145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ala Ala Cys
165 170 175

Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr
180 185 190

Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr

210

215

220

Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
225 230 235 240

Asn Val Ala Val Lys Glu Ser Ser Asn Ala
245 250

<210> 16

<211> 753

<212> DNA

<213> Naturally occurring gamma prtoeobacterium

<220>

<221> CDS

<222> (1)..(753)

<223> Proteorhodopsin variant from pcr clone HOT75m1: GenBank#AF349979

<400> 16

atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca 48
Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
1 5 10 15

ttt gct gct gct ggt ggc gat cta gat ata agt gat act gtt ggt gtt 96
Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
20 25 30

tca ttc tgg ctg gtt aca gct ggt atg tta gcg gca act gtg ttc ttt 144
Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
35 40 45

ttt gta gaa aga gac caa gtc agc gct aag tgg aaa act tca ctt gct 192
Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Ala
50 55 60

gta tct ggt tta att act ggt ata gct ttt tgg cat tat ctc tat atg Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met 65 70 75 80	240
aga ggt gtt tgg ata gac act ggt gat acc cca aca gta ttc aga tat Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr 85 90 95	288
att gat tgg tta tta act gtt cca tta caa atg gtt gag ttc tat cta Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu 100 105 110	336
att ctt gct gct tgt aca agt gtt gct gct tca tta ttt aag aag ctt Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu 115 120 125	384
cta gct ggt tca tta gta atg tta ggt gct gga ttt gca ggc gaa gct Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala 130 135 140	432
gga tta gct cct gta tta cct gct ttc att att ggt atg gct gga tgg Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp 145 150 155 160	480
tta tac atg att tat gag cta tat atg ggt gaa ggt aag gct gct gta Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val 165 170 175	528
agt act gca agt cct gct gtt aac tct gca tac aac gca atg atg atg Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Met 180 185 190	576
att att gtt gtt gga tgg gca att tat cct gct gga tat gct gct ggt Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly 195 200 205	624
tac cta atg ggt ggc gaa ggt gta tac gct tca aac tta aac ctt ata Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile 210 215 220	672
tat aac ctt gcc gac ctt gtt aac aag att cta ttt ggt ttg atc att Tyr Asn Leu Ala Asp Leu Val Asn Lys Ile Leu Phe Gly Leu Ile Ile 225 230 235 240	720
tgg aat gtt gct gtt aaa gaa tct tct aat gct Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala 245 250	753

<210> 17

<211> 251

<212> PRT

<213> Naturally occurring gamma prtoeobacterium

<400> 17

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
1 5 10 15

Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
20 25 30

Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
35 40 45

Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Ala
50 55 60

Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
65 70 75 80

Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
100 105 110

Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu
115 120 125

Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
130 135 140

Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp
 145 150 155 160

Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val
 165 170 175

Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Met
 180 185 190

Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
 195 200 205

Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
 210 215 220

Tyr Asn Leu Ala Asp Leu Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
 225 230 235 240

Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 18

<211> 753

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(753)

<223> Proteorhodopsin variant from pcr clone HOT75m3; GenBank#AF349980

<400> 18																
atg	ggt	aaa	tta	tta	ctg	ata	tta	ggt	agt	gct	att	gca	ctt	cca	tca	48
Met	Gly	Lys	Leu	Leu	Leu	Ile	Leu	Gly	Ser	Ala	Ile	Ala	Leu	Pro	Ser	
1				5					10					15		
ttt	gct	gct	gct	ggt	ggc	gat	cta	gat	ata	agt	gat	act	gtt	ggt	gtt	96
Phe	Ala	Ala	Ala	Gly	Gly	Asp	Leu	Asp	Ile	Ser	Asp	Thr	Val	Gly	Val	
			20					25					30			
tca	ttc	tgg	ctg	gtt	aca	gct	ggt	atg	tta	gcg	gca	act	gta	ttc	ttt	144
Ser	Phe	Trp	Leu	Val	Thr	Ala	Gly	Met	Leu	Ala	Ala	Thr	Val	Phe	Phe	
		35					40					45				
ttt	gta	gaa	aga	gac	caa	gtc	agc	gct	aag	tgg	aaa	act	tca	ctt	act	192
Phe	Val	Glu	Arg	Asp	Gln	Val	Ser	Ala	Lys	Trp	Lys	Thr	Ser	Leu	Thr	
	50					55					60					
gta	tct	ggt	tta	att	act	ggt	ata	gct	ttt	tgg	cat	tat	ctc	tac	atg	240
Val	Ser	Gly	Leu	Ile	Thr	Gly	Ile	Ala	Phe	Trp	His	Tyr	Leu	Tyr	Met	
65					70					75					80	
aga	ggt	gtt	tgg	ata	gat	act	ggt	gat	aca	cca	aca	gta	ttt	aga	tat	288
Arg	Gly	Val	Trp	Ile	Asp	Thr	Gly	Asp	Thr	Pro	Thr	Val	Phe	Arg	Tyr	
				85					90					95		
att	gat	tgg	tta	tta	act	gtt	cca	tta	caa	atg	gtt	gag	ttc	tat	cta	336
Ile	Asp	Trp	Leu	Leu	Thr	Val	Pro	Leu	Gln	Met	Val	Glu	Phe	Tyr	Leu	
			100					105					110			
att	ctt	gct	gct	tgt	aca	agt	gtt	gct	gct	tca	tta	ttt	aag	aag	ctt	384
Ile	Leu	Ala	Ala	Cys	Thr	Ser	Val	Ala	Ala	Ser	Leu	Phe	Lys	Lys	Leu	
		115					120					125				
cta	gct	ggt	tca	tta	gta	atg	tta	ggt	gct	gga	ttt	gca	ggc	gaa	gct	432
Leu	Ala	Gly	Ser	Leu	Val	Met	Leu	Gly	Ala	Gly	Phe	Ala	Gly	Glu	Ala	
	130					135					140					
ggt	tta	gct	cct	gta	tta	cct	gct	ttc	att	att	ggt	atg	gct	gga	tgg	480
Gly	Leu	Ala	Pro	Val	Leu	Pro	Ala	Phe	Ile	Ile	Gly	Met	Ala	Gly	Trp	
145					150					155					160	
tta	tac	atg	att	tat	gag	cta	cat	atg	ggt	gaa	ggt	aag	gct	gct	gta	528
Leu	Tyr	Met	Ile	Tyr	Glu	Leu	His	Met	Gly	Glu	Gly	Lys	Ala	Ala	Val	
				165					170					175		

agt act gca agt cct gct gtt aac tct gca tac aac gca atg atg aag 576
 Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Lys
 180 185 190

att att gtt att gga tgg gca att tat cct gct gga tat gct gct ggt 624
 Ile Ile Val Ile Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
 195 200 205

tac cta atg agt ggt gac ggt gta tac gct tca aac tta aac ctt ata 672
 Tyr Leu Met Ser Gly Asp Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
 210 215 220

tat aac ctt gct gac ttt gtt aac aag att cta ttt ggt ttg atc att 720
 Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
 225 230 235 240

tgg aat gtt gct gtt aaa gaa tct tct aat gct 753
 Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 19

<211> 251

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 19

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
 1 5 10 15

Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
 20 25 30

Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
 35 40 45

Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60

<210> 20

<211> 753

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(753)

<223> Proteorhodopsin variant from pcr clone HOT75m4; GenBank #AF349981

<400> 20

atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca	48
Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser	
1 5 10 15	
ttt gct gct gct ggt ggc gat cta gat ata agt gat act gtt ggt gtt	96
Phe Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val	
20 25 30	
tca ttc tgg ctg gtt aca gct ggt atg tta gcg gca act gtg ttc ttt	144
Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe	
35 40 45	
ttt gta gaa aga gac caa gtc agc gct aag tgg aaa act tca ctt act	192
Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr	
50 55 60	
gta tct ggt tta att act ggt ata gct ttt tgg cat tat ctc tat atg	240
Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met	
65 70 75 80	
aga ggt gtt tgg ata gac act ggt gat acc cca aca gta ttc aga tat	288
Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr	
85 90 95	
att gat tgg tta tta act gtt cca tta caa gtg gtt gag ttc tat cta	336
Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Val Val Glu Phe Tyr Leu	

100	105	110	
att ctt gct gct tgt aca agt gtt gct gct tca tta ttt aag aag ctt			384
Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu			
115	120	125	
cta gct ggt tca tta gta atg tta ggt gct gga ttt gca ggc gaa gct			432
Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala			
130	135	140	
gga tta gct cct gta tta cct gct ttc att att ggt atg gct gga tgg			480
Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp			
145	150	155	160
tta tac atg att tat gag cta tat atg ggt gaa ggt aag gct gct gta			528
Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val			
	165	170	175
agt act gca agt cct gct gtt aac tct gca tac aac gca atg atg atg			576
Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Met			
	180	185	190
att att gtt gtt gga tgg gca att tat cct gct gga tat gct gct ggt			624
Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly			
	195	200	205
tac cta atg ggt ggc gaa ggt gta tac gct tca aac tta aac ctt ata			672
Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile			
	210	215	220
tat aac ctt gct gac ttt gtt aac aag att cta ttt ggt ttg atc att			720
Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile			
225	230	235	240
tgg aat gtt gct gtt aaa gaa tct tct aat gct			753
Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala			
	245	250	

<210> 21

<211> 251

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 21

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
1 5 10 15

Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
20 25 30

Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
35 40 45

Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50 55 60

Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
65 70 75 80

Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Val Val Glu Phe Tyr Leu
100 105 110

Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu
115 120 125

Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
130 135 140

Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp
145 150 155 160

Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val
165 170 175

Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Met
 180 185 190

Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
 195 200 205

Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
 210 215 220

Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
 225 230 235 240

Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 22

<211> 753

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(753)

<223> Proteorhodopsin variant from pcr clone HOT75m8: GenBank#AF349982

<400> 22

atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca 48
 Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
 1 5 10 15

ttt gct gct gct ggt ggc gat cta gat ata agt gat act gtt ggt gtt 96
 Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val

	20					25					30					
tca ttc tgg ctg gtt aca gct ggt atg tta gcg gca act gtg ttc ttt																144
Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe																
	35					40					45					
ttt gta gaa aga gac caa gtc agc gct aag tgg aaa act tca ctt act																192
Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr																
	50					55					60					
gta tct ggt tta att act ggt ata gct ttt tgg cat tat ctc tat atg																240
Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met																
	65					70					75					80
aga ggt gtt tgg ata gac act ggt gat acc cca aca gta ttc aga tat																288
Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr																
	85					90					95					
att gat tgg tta tta act gtt cca tta caa atg gtt gag ttc tat cta																336
Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu																
	100					105					110					
att ctt gct gct tgt aca aat gtt gct gct tca tta ttt aag aag ctt																384
Ile Leu Ala Ala Cys Thr Asn Val Ala Ala Ser Leu Phe Lys Lys Leu																
	115					120					125					
cta gct ggt tca tta gta atg tta ggt gct gga ttt gca ggc gaa gct																432
Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala																
	130					135					140					
gga ttg gct cct gta tgg cct gct ttc att att ggt atg gct gga tgg																480
Gly Leu Ala Pro Val Trp Pro Ala Phe Ile Ile Gly Met Ala Gly Trp																
	145					150					155					160
tta tac atg att tat gag cta tat atg ggt gaa ggt aag gct gct gta																528
Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val																
	165					170					175					
agt act gca agt cct gct gtt aac tct gca tac aac gca atg atg gtg																576
Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Val																
	180					185					190					
att att gtt gtt gga tgg gca att tat cct gct gga tat gct gct ggt																624
Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly																
	195					200					205					
tac cta atg ggt ggc gaa ggt gta tac gct tca aac tta aac ctt ata																672
Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile																

210		215		220	
tat aac ctt gcc gac ctt gtt aac aag att cta ttt ggt ttg atc att					720
Tyr Asn Leu Ala Asp Leu Val Asn Lys Ile Leu Phe Gly Leu Ile Ile					
225		230		235	240

tgg aat gtt gct gtt aaa gaa tct tct aat gct					753
Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala					
	245			250	

<210> 23

<211> 251

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 23

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
1 5 10 15

Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
20 25 30

Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
35 40 45

Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50 55 60

Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
65 70 75 80

Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu

100 105 110

Ile Leu Ala Ala Cys Thr Asn Val Ala Ala Ser Leu Phe Lys Lys Leu
115 120 125

Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
130 135 140

Gly Leu Ala Pro Val Trp Pro Ala Phe Ile Ile Gly Met Ala Gly Trp
145 150 155 160

Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val
165 170 175

Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Val
180 185 190

Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
195 200 205

Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
210 215 220

Tyr Asn Leu Ala Asp Leu Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
225 230 235 240

Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
245 250

<210> 24

<211> 750

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(750)

<223> Proteorhodopsin variant from pcr clone MB0m1: GenBank#AF349983

<400> 24

atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca 48
Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
1 5 10 15

ttt gct gca ggt ggt ggt gac ctt gat gct agt gat tac act ggt gtt 96
Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
20 25 30

tct ttt tgg tta gtt act gct gct cta tta gca tct act gta ttt ttc 144
Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
35 40 45

ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act 192
Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50 55 60

gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg 240
Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
65 70 75 80

tga ggg gta tgg att gag act ggt gat tcg cca act gta ttt aga tac 288
Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
85 90 95

att gat tgg tta cta aca gtt cct cta ttg ata tgt gaa ttc tac tta 336
Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
100 105 110

att ctt gct gct gca aca aat gtt gct gct ggc ctg ttt aag aaa tta 384
Ile Leu Ala Ala Ala Thr Asn Val Ala Ala Gly Leu Phe Lys Lys Leu
115 120 125

ttg gtt ggt tct ctt gtt atg ctt gtg ttt ggt tac atg ggt gag gca 432
Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
130 135 140

gga att atg aac gct tgg cct gca ttc att att ggg tgt tta gct tgg 480
 Gly Ile Met Asn Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp
 145 150 155 160

gta tac atg att tat gaa cta tat gct gga gaa gga aaa tct gca tgt 528
 Val Tyr Met Ile Tyr Glu Leu Tyr Ala Gly Glu Gly Lys Ser Ala Cys
 165 170 175

aat act gca agt cct tcg gtt caa tca gct tac aac aca atg atg gct 576
 Asn Thr Ala Ser Pro Ser Val Gln Ser Ala Tyr Asn Thr Met Met Ala
 180 185 190

atc ata gtc ttc ggt tgg gca att tat cct gta ggt tat ttc aca ggt 624
 Ile Ile Val Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
 195 200 205

tac cta atg ggt gac ggt gga tca gct ctt aac tta aac ctt att tat 672
 Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
 210 215 220

aac ctt gct gac ttt gtt aac aag att cta ttt ggt tta att ata tgg 720
 Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
 225 230 235 240

aat gtt gct gtt aaa gaa tct tct aat gct 750
 Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 25

<211> 250

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 25

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 1 5 10 15

Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30

Val 65	Ser	Gly	Leu	Val	Thr 70	Gly	Ile	Ala	Phe	Trp 75	His	Tyr	Met	Tyr	Met 80	
aga	ggg	gta	tgg	att	gaa	act	ggg	gat	tcg	cca	act	gta	ttt	aga	tac	288
Arg	Gly	Val	Trp	Ile	Glu	Thr	Gly	Asp	Ser	Pro	Thr	Val	Phe	Arg	Tyr	
				85					90					95		
att	gat	tgg	tta	cta	aca	ggt	cct	cta	tta	ata	tgt	gaa	ttc	tac	tta	336
Ile	Asp	Trp	Leu	Leu	Thr	Val	Pro	Leu	Leu	Ile	Cys	Glu	Phe	Tyr	Leu	
			100					105					110			
att	ctt	gct	gct	gct	act	aat	ggt	gct	gct	ggc	ctg	ttt	aag	aaa	tta	384
Ile	Leu	Ala	Ala	Ala	Thr	Asn	Val	Ala	Ala	Gly	Leu	Phe	Lys	Lys	Leu	
		115					120					125				
ttg	gtt	ggg	tct	ctt	gtt	atg	ctt	gtg	ttt	ggg	tac	atg	ggg	gaa	gca	432
Leu	Val	Gly	Ser	Leu	Val	Met	Leu	Val	Phe	Gly	Tyr	Met	Gly	Glu	Ala	
	130					135					140					
gga	att	atg	aac	gct	tgg	ggg	gca	ttc	gtt	att	ggg	tgt	tta	gct	tgg	480
Gly	Ile	Met	Asn	Ala	Trp	Gly	Ala	Phe	Val	Ile	Gly	Cys	Leu	Ala	Trp	
145					150					155					160	
gta	tac	atg	att	tat	gag	ctt	tgg	ctt	gga	gaa	gga	aaa	gct	gcg	tgt	528
Val	Tyr	Met	Ile	Tyr	Glu	Leu	Trp	Leu	Gly	Glu	Gly	Lys	Ala	Ala	Cys	
				165					170					175		
aat	aca	gca	agt	cct	gct	gtt	cag	tca	gct	tac	aac	aca	atg	atg	atg	576
Asn	Thr	Ala	Ser	Pro	Ala	Val	Gln	Ser	Ala	Tyr	Asn	Thr	Met	Met	Met	
			180					185					190			
atc	atc	atc	ttt	ggg	tgg	gca	att	tat	cct	gta	ggg	tat	ttc	aca	ggg	624
Ile	Ile	Ile	Phe	Gly	Trp	Ala	Ile	Tyr	Pro	Val	Gly	Tyr	Phe	Thr	Gly	
			195				200					205				
tac	cta	atg	ggg	gac	ggg	gga	tca	gca	ctt	aac	tta	aac	ctt	atc	tat	672
Tyr	Leu	Met	Gly	Asp	Gly	Gly	Ser	Ala	Leu	Asn	Leu	Asn	Leu	Ile	Tyr	
	210					215					220					
aac	ctt	gct	gac	ttt	gtt	aac	aag	att	cta	ttt	ggg	tta	att	ata	tgg	720
Asn	Leu	Ala	Asp	Phe	Val	Asn	Lys	Ile	Leu	Phe	Gly	Leu	Ile	Ile	Trp	
225					230					235					240	
aat	gtt	gct	gtt	aaa	gaa	tct	tct	aat	gct							750
Asn	Val	Ala	Val	Lys	Glu	Ser	Ser	Asn	Ala							
				245					250							

<210> 27

<211> 250

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 27

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
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Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
20 25 30

Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
35 40 45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
100 105 110

Ile Leu Ala Ala Ala Thr Asn Val Ala Ala Gly Leu Phe Lys Lys Leu
115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
130 135 140

Gly Ile Met Asn Ala Trp Gly Ala Phe Val Ile Gly Cys Leu Ala Trp
 145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Trp Leu Gly Glu Gly Lys Ala Ala Cys
 165 170 175

Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Met
 180 185 190

Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
 195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
 210 215 220

Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
 225 230 235 240

Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 28

<211> 750

<212> DNA

<213> Naturally occuring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(750)

<223> Proteorhodopsin variant from pcr clone MB20m2; GenBank #AF349985

Table 1. Demographic characteristics of the study population	
Age (years)	Mean (SD)
Male	50.5 (10.5)
Female	51.5 (10.5)
Marital status	
Married	75.5%
Single	24.5%
Education level	
High school or above	65.5%
Below high school	34.5%
Occupation	
Professional	15.5%
Managerial	10.5%
Technical	15.5%
Service	25.5%
Skilled	15.5%
Unskilled	17.5%
Health status	
Good	75.5%
Fair	15.5%
Poor	9.0%
Smoking status	
Smoker	25.5%
Non-smoker	74.5%
Alcohol consumption	
Drinker	15.5%
Non-drinker	84.5%
Family size	
1-2	35.5%
3-4	45.5%
5 or more	19.0%
Income (US\$)	
<1000	15.5%
1000-2000	35.5%
2000-3000	25.5%
>3000	23.5%

Page 120

Asn	Thr	Ala	Ser	Pro	Ala	Val	Gln	Ser	Ala	Tyr	Asn	Thr	Met	Met	Tyr	
			180					185					190			
ata	atc	atc	ttt	ggt	tgg	gca	att	tat	cct	gta	ggt	tat	ttc	aca	ggt	624
Ile	Ile	Ile	Phe	Gly	Trp	Ala	Ile	Tyr	Pro	Val	Gly	Tyr	Phe	Thr	Gly	
			195				200					205				
tac	cta	atg	ggt	gac	ggt	gga	tca	gct	ctt	aac	tta	aac	ctt	atc	tat	672
Tyr	Leu	Met	Gly	Asp	Gly	Gly	Ser	Ala	Leu	Asn	Leu	Asn	Leu	Ile	Tyr	
	210					215					220					
aac	ctt	gct	gac	ttt	gtt	aac	aag	att	cta	ttt	ggt	tta	att	ata	tgg	720
Asn	Leu	Ala	Asp	Phe	Val	Asn	Lys	Ile	Leu	Phe	Gly	Leu	Ile	Ile	Trp	
225					230					235					240	
aat	gtt	gct	gtt	aaa	gaa	tct	tct	aat	gct							750
Asn	Val	Ala	Val	Lys	Glu	Ser	Ser	Asn	Ala							
				245					250							

<210> 29

<211> 250

<212> PRT

<213> Naturally occuring gamma proteobacterium

<400> 29

Met	Gly	Lys	Leu	Leu	Leu	Ile	Leu	Gly	Ser	Val	Ile	Ala	Leu	Pro	Thr
1				5					10					15	

Phe	Ala	Ala	Gly	Gly	Gly	Asp	Leu	Asp	Ala	Ser	Asp	Tyr	Thr	Gly	Val
			20					25					30		

Ser	Phe	Trp	Leu	Val	Thr	Ala	Ala	Leu	Leu	Ala	Ser	Thr	Val	Phe	Phe
		35					40					45			

Phe	Val	Glu	Arg	Asp	Arg	Val	Ser	Ala	Lys	Trp	Lys	Thr	Ser	Leu	Thr
	50					55					60				

Val	Ser	Gly	Leu	Val	Thr	Gly	Ile	Ala	Phe	Trp	His	Tyr	Met	Tyr	Met	65	70	75	80
Arg	Gly	Val	Trp	Ile	Glu	Thr	Gly	Asp	Ser	Pro	Thr	Val	Phe	Arg	Tyr	85	90	95	
Ile	Asp	Trp	Leu	Leu	Thr	Val	Pro	Leu	Leu	Ile	Cys	Glu	Phe	Tyr	Leu	100	105	110	
Ile	Leu	Ala	Ala	Ala	Thr	Asn	Val	Ala	Ala	Gly	Leu	Phe	Lys	Lys	Leu	115	120	125	
Leu	Val	Gly	Ser	Leu	Val	Met	Leu	Val	Phe	Gly	Tyr	Met	Gly	Glu	Ala	130	135	140	
Gly	Ile	Met	Asn	Ala	Trp	Gly	Ala	Phe	Val	Ile	Gly	Cys	Leu	Ala	Trp	145	150	155	160
Val	Tyr	Met	Ile	Tyr	Glu	Leu	Trp	Ala	Gly	Glu	Gly	Lys	Ala	Ala	Cys	165	170	175	
Asn	Thr	Ala	Ser	Pro	Ala	Val	Gln	Ser	Ala	Tyr	Asn	Thr	Met	Met	Tyr	180	185	190	
Ile	Ile	Ile	Phe	Gly	Trp	Ala	Ile	Tyr	Pro	Val	Gly	Tyr	Phe	Thr	Gly	195	200	205	
Tyr	Leu	Met	Gly	Asp	Gly	Gly	Ser	Ala	Leu	Asn	Leu	Asn	Leu	Ile	Tyr	210	215	220	
Asn	Leu	Ala	Asp	Phe	Val	Asn	Lys	Ile	Leu	Phe	Gly	Leu	Ile	Ile	Trp	225	230	235	240
Asn	Val	Ala	Val	Lys	Glu	Ser	Ser	Asn	Ala							245	250		

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<210> 30
<211> 750
<212> DNA
<213> Naturally occurring gamma proteobacterium

<220>
<221> CDS
<222> (1)..(750)
<223> Proteorhodopsin variant from pcr clone MB20m5; GenBank#AF349986

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Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
1          5          10          15

ttt gct gca ggt ggc ggt gac ctt gat gct agt gat tac act ggt gtt      96
Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
          20          25          30

tct ttt tgg tta gtt aca gct gct cta tta gca tct act gta ttt ttc      144
Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
          35          40          45

ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act      192
Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
          50          55          60

gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg      240
Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
65          70          75          80

aga ggg gta tgg att gaa act ggt gat tcg cca act gta ttt aga tac      288
Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
          85          90          95

att gat tgg tta cta aca gtt cct cta tta ata tgt gaa ttc tac tta      336
Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
          100          105          110

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<400> 31

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
1 5 10 15

Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
20 25 30

Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
35 40 45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
100 105 110

Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu
115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
130 135 140

Gln Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp
145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Tyr Ala Gly Glu Gly Lys Ser Ala Cys
165 170 175

Asn Thr Ala Ser Pro Ser Val Gln Ser Ala Tyr Asn Thr Met Met Ala
180 185 190

Ile Ile Val Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
210 215 220

Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Leu Gly Leu Ile Ile Trp
225 230 235 240

Asn Val Ala Val Lys Glu Ser Ser Asn Ala
245 250

<210> 32

<211> 750

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(750)

<223> Proteorhodopsin variant from pcr clone MB20m12; GenBank #AF349987

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Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr	
1 5 10 15	

ttt gct gca ggt ggt ggt gac ctt gat gct agt gat tac act ggt gtt	96
Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val	
20 25 30	

tct ttt tgg tta gtt act gct gct tta tta gca tct act gta ttt ttc	144
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Ser	Phe	Trp	Leu	Val	Thr	Ala	Ala	Leu	Leu	Ala	Ser	Thr	Val	Phe	Phe		
		35					40					45					
ttt	ggt	gaa	aga	gat	aga	ggt	tct	gca	aaa	tgg	aaa	aca	tca	tta	act		192
Phe	Val	Glu	Arg	Asp	Arg	Val	Ser	Ala	Lys	Trp	Lys	Thr	Ser	Leu	Thr		
	50					55				60							
gta	tct	ggt	ctt	ggt	act	ggt	att	gct	ttc	tgg	cat	tac	atg	tac	atg		240
Val	Ser	Gly	Leu	Val	Thr	Gly	Ile	Ala	Phe	Trp	His	Tyr	Met	Tyr	Met		
65					70					75					80		
aga	ggg	gta	tgg	att	gaa	act	ggt	gat	tcg	cca	act	gta	ttt	aga	tac		288
Arg	Gly	Val	Trp	Ile	Glu	Thr	Gly	Asp	Ser	Pro	Thr	Val	Phe	Arg	Tyr		
				85				90					95				
att	gat	tgg	tta	cta	aca	ggt	cct	cta	tta	ata	tgt	gaa	ttc	tac	tta		336
Ile	Asp	Trp	Leu	Leu	Thr	Val	Pro	Leu	Leu	Ile	Cys	Glu	Phe	Tyr	Leu		
			100					105					110				
att	ctt	gct	gct	gca	gct	aat	ggt	gct	gga	tca	tta	ttt	aag	aaa	tta		384
Ile	Leu	Ala	Ala	Ala	Ala	Asn	Val	Ala	Gly	Ser	Leu	Phe	Lys	Lys	Leu		
		115					120					125					
cta	ggt	ggt	tct	ctt	ggt	atg	ctt	gtg	ttt	ggt	tac	atg	ggt	gaa	gca		432
Leu	Val	Gly	Ser	Leu	Val	Met	Leu	Val	Phe	Gly	Tyr	Met	Gly	Glu	Ala		
	130					135					140						
gga	atc	atg	gct	gca	tgg	cct	gca	ttc	att	att	ggg	tgt	tta	gct	tgg		480
Gly	Ile	Met	Ala	Ala	Trp	Pro	Ala	Phe	Ile	Ile	Gly	Cys	Leu	Ala	Trp		
145					150					155					160		
gta	tac	atg	att	tat	gaa	tta	tgg	gct	gga	gaa	gga	aaa	tct	gca	tgt		528
Val	Tyr	Met	Ile	Tyr	Glu	Leu	Trp	Ala	Gly	Glu	Gly	Lys	Ser	Ala	Cys		
				165				170						175			
aat	act	gca	agt	cct	gct	gtg	caa	tca	gcc	tac	aac	aca	atg	atg	tat		576
Asn	Thr	Ala	Ser	Pro	Ala	Val	Gln	Ser	Ala	Tyr	Asn	Thr	Met	Met	Tyr		
			180					185					190				
att	atc	atc	ttt	ggt	tgg	gcg	att	tat	cct	gta	ggt	tat	ttc	aca	ggt		624
Ile	Ile	Ile	Phe	Gly	Trp	Ala	Ile	Tyr	Pro	Val	Gly	Tyr	Phe	Thr	Gly		
		195					200				205						
tac	ttg	atg	ggt	gac	ggt	gga	tca	gct	ctt	aac	tta	aac	ctt	atc	tat		672
Tyr	Leu	Met	Gly	Asp	Gly	Gly	Ser	Ala	Leu	Asn	Leu	Asn	Leu	Ile	Tyr		
	210					215					220						
aac	ctt	gct	gac	ttt	ggt	aac	aag	att	cta	ttt	ggt	tta	att	ata	tgg		720

Ile Leu Ala Ala Ala Asn Val Ala Gly Ser Leu Phe Lys Lys Leu
115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
130 135 140

Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp
145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys
165 170 175

Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr
180 185 190

Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
210 215 220

Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
225 230 235 240

Asn Val Ala Val Lys Glu Ser Ser Asn Ala
245 250

<210> 34

<211> 750

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(750)

<223> Proteorhodopsin variant from pcr clone MB40m1; GenBank #AF349988

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1 5 10 15	
ttt gct gca ggt ggc ggt gac ctt gat gct agt gat tac act ggt gtt	96
Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val	
20 25 30	
tct ttt tgg tta gtt aca gct gct cta tta gca tct act gta ttt ttc	144
Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe	
35 40 45	
ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act	192
Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr	
50 55 60	
gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg	240
Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met	
65 70 75 80	
aga gga gta tgg att gaa act ggt gat tcg cca act gta ttt aga tac	288
Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr	
85 90 95	
att gat tgg tta cta aca gtt cct tta tta ata tgt gaa ttc tac tta	336
Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu	
100 105 110	
att ctt gct gct gca act aat gtt gcc ggc tca tta ttt aag aaa ctt	384
Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu	
115 120 125	
cta gtt ggt tct ctt gtt atg ctt gtg ttt ggt tac atg ggt gaa gca	432
Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala	
130 135 140	
gga att atg gca gct tgg cct gca ttc att att ggg tgt tta gct tgg	480
Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp	

145									150									155									160									
gta	tat	atg	att	tat	gaa	cta	tat	gct	gga	gaa	gga	aaa	tct	gca	tgt		528																			
Val	Tyr	Met	Ile	Tyr	Glu	Leu	Tyr	Ala	Gly	Glu	Gly	Lys	Ser	Ala	Cys																					
				165					170					175																						
aat	aca	gca	agt	cct	gct	gtg	caa	tca	gct	tac	aac	aca	atg	atg	tat		576																			
Asn	Thr	Ala	Ser	Pro	Ala	Val	Gln	Ser	Ala	Tyr	Asn	Thr	Met	Met	Tyr																					
				180					185					190																						
att	atc	gtc	ttt	ggc	tgg	gcg	att	tat	cct	gta	ggc	tat	ttc	aca	ggc		624																			
Ile	Ile	Val	Phe	Gly	Trp	Ala	Ile	Tyr	Pro	Val	Gly	Tyr	Phe	Thr	Gly																					
				195					200					205																						
tac	ctg	atg	ggc	gac	ggc	gga	tca	gct	ctt	aac	tta	aac	ctt	atc	tat		672																			
Tyr	Leu	Met	Gly	Asp	Gly	Gly	Ser	Ala	Leu	Asn	Leu	Asn	Leu	Ile	Tyr																					
				210					215					220																						
aac	ctt	gct	gac	ttt	gtt	aac	aag	att	cta	ttt	ggc	tta	att	ata	tgg		720																			
Asn	Leu	Ala	Asp	Phe	Val	Asn	Lys	Ile	Leu	Phe	Gly	Leu	Ile	Ile	Trp																					
				225					230					235					240																	
aat	gtt	gct	gtt	aaa	gaa	tct	tct	aat	gct									750																		
Asn	Val	Ala	Val	Lys	Glu	Ser	Ser	Asn	Ala																											
				245					250																											

<210> 35

<211> 250

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 35

Met Gly Lys Leu Leu Leu Ile Ile Gly Ser Val Ile Ala Leu Pro Thr
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Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
20 25 30

Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe

Protein Data Bank

35

40

45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
100 105 110

Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu
115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
130 135 140

Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp
145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Tyr Ala Gly Glu Gly Lys Ser Ala Cys
165 170 175

Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr
180 185 190

Ile Ile Val Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
210 215 220

Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp

aga ggg gta tgg att gag act ggt gat tcg cca act gta ttt aga tac	288
Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr	
85 90 95	
att gat tgg tta cta aca gtt cct cta ttg ata tgt gaa ttc tac tta	336
Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu	
100 105 110	
att ctt gct gct gca aca aat gtt gct gct ggc ctg ttt aag aaa tta	384
Ile Leu Ala Ala Thr Asn Val Ala Ala Gly Leu Phe Lys Lys Leu	
115 120 125	
ttg gtt ggt tct ctt gtt atg ctt gtg ttt ggt tac atg ggt gag gca	432
Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala	
130 135 140	
gga att atg aac gct tgg ggt gca ttc gtt att ggg tgt tta gct tgg	480
Gly Ile Met Asn Ala Trp Gly Ala Phe Val Ile Gly Cys Leu Ala Trp	
145 150 155 160	
gta tac atg att tat gaa cta tgg gct gga gaa ggc aag gct gca tgt	528
Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ala Ala Cys	
165 170 175	
aat act gca agt cct gct gtg caa tca gct tac aac aca atg atg tat	576
Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr	
180 185 190	
ata atc atc ttt ggt tgg gca att tat cct gta ggt tat ttc aca ggt	624
Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly	
195 200 205	
tac cta atg ggt gac ggt gga tca gct ctt aac tta aac ctt atc tat	672
Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr	
210 215 220	
aac ctt gct gac ttt gtt aac aag aat cta ttt ggt tta att ata tgg	720
Asn Leu Ala Asp Phe Val Asn Lys Asn Leu Phe Gly Leu Ile Ile Trp	
225 230 235 240	
aat gtt gct gtt aaa gaa tct tct aat gct	750
Asn Val Ala Val Lys Glu Ser Ser Asn Ala	
245 250	

<210> 37

<211> 250

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 37

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
1 5 10 15

Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
20 25 30

Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
35 40 45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
100 105 110

Ile Leu Ala Ala Ala Thr Asn Val Ala Ala Gly Leu Phe Lys Lys Leu
115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
130 135 140

Gly Ile Met Asn Ala Trp Gly Ala Phe Val Ile Gly Cys Leu Ala Trp
145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ala Ala Cys
165 170 175

Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr
180 185 190

Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
210 215 220

Asn Leu Ala Asp Phe Val Asn Lys Asn Leu Phe Gly Leu Ile Ile Trp
225 230 235 240

Asn Val Ala Val Lys Glu Ser Ser Asn Ala
245 250

<210> 38

<211> 750

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(750)

<223> Proteorhodopsin variant from pcr clone MB40m12; GenBank # AF34999

<400> 38

atg ggt aaa tta tta cgg ata tta ggt agt gtt att gca ctt cct aca Met Gly Lys Leu Leu Arg Ile Leu Gly Ser Val Ile Ala Leu Pro Thr 1 5 10 15	48
ttt gct gca ggt ggc ggt gac ctt gat gct agt gat tac act ggt gtt Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val 20 25 30	96
tct ttt tgg tta gtt aca gct gct cta tta gca tct act gta ttt ttc Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe 35 40 45	144
ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr 50 55 60	192
gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tat atg Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met 65 70 75 80	240
aga gga gta tgg att gaa act ggt gat tcg cca act gta ttt aga tac Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr 85 90 95	288
att gat tgg tta cta aca gtt cct tta tta ata tgt gaa ttc tac tta Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu 100 105 110	336
att ctt gct gct gca act aat gtt gct gga tca tta ttt aag aaa tta Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu 115 120 125	384
cta gtt ggt tct ctt gtt atg ctt gtg ttt ggt tac atg ggt gaa gca Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala 130 135 140	432
gga atc atg gct gca tgg cct gca ttc att att ggg tgt tta gct tgg Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp 145 150 155 160	480
gta tac atg att tat gaa cta tgg gct gga gaa gga aaa tct gca tgt Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys 165 170 175	528
aat act gca agt cct gct gtg caa tca gct tac aac aca atg atg tat Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr 180 185 190	576

atc atc atc gtt ggt tgg gcg att tat cct gta ggt tat ttc aca ggt 624
 Ile Ile Ile Val Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
 195 200 205

tac ctg atg ggt gac ggt gga tca gct ctt aac tta aac ctt atc tat 672
 Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
 210 215 220

aac ctt gct gac ttt gtt aac aag att cta ttt ggt tta att ata tgg 720
 Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
 225 230 235 240

aat gtt gct gtt aaa gaa tct tct aat gct 750
 Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 39

<211> 250

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 39

Met Gly Lys Leu Leu Arg Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
 1 5 10 15

Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30

Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
 65 70 75 80

<211> 750

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(750)

<223> Proteorhodopsin variant from pcr clone MB100m5; GenBank #AF349991

<400> 40

atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca	48
Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr	
1 5 10 15	
ttt gct gca ggt ggc ggt gac ctt gat gct agt gat tac act ggt gtt	96
Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val	
20 25 30	
tct ttt tgg tta gtt aca gct gct cta tta gca tct act gta ttt ttc	144
Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe	
35 40 45	
ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act	192
Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr	
50 55 60	
gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg	240
Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met	
65 70 75 80	
aga gga gta tgg att gaa act ggt gat tcg cca act gta ttt aga tac	288
Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr	
85 90 95	
att gat tgg tta cta aca gtt cct tta tta ata tgt gaa ttc tac tta	336
Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu	
100 105 110	
att ctt gct gct gca act aat gtt gcc ggc tca tta ttt aag aaa ctt	384

Ile	Leu	Ala	Ala	Ala	Thr	Asn	Val	Ala	Gly	Ser	Leu	Phe	Lys	Lys	Leu		
		115					120					125					
cta	gtt	ggt	tct	ctt	gtt	atg	ctt	gtg	ttt	ggt	tac	atg	ggt	gaa	gca		432
Leu	Val	Gly	Ser	Leu	Val	Met	Leu	Val	Phe	Gly	Tyr	Met	Gly	Glu	Ala		
	130					135					140						
gga	att	atg	gca	gct	tgg	cct	gca	ttc	att	att	ggg	tgt	tta	gct	tgg		480
Gly	Ile	Met	Ala	Ala	Trp	Pro	Ala	Phe	Ile	Ile	Gly	Cys	Leu	Ala	Trp		
145					150					155					160		
gta	tac	atg	att	tat	gaa	cta	tat	gct	gga	gaa	gga	aaa	tct	gca	tgt		528
Val	Tyr	Met	Ile	Tyr	Glu	Leu	Tyr	Ala	Gly	Glu	Gly	Lys	Ser	Ala	Cys		
				165					170					175			
aat	act	gca	agt	cct	tcg	gtt	caa	tca	gct	tac	aac	aca	atg	atg	gct		576
Asn	Thr	Ala	Ser	Pro	Ser	Val	Gln	Ser	Ala	Tyr	Asn	Thr	Met	Met	Ala		
			180					185					190				
atc	ata	gtc	ttc	ggg	tgg	gca	att	tat	cct	gta	ggt	tat	ttc	aca	ggg		624
Ile	Ile	Val	Phe	Gly	Trp	Ala	Ile	Tyr	Pro	Val	Gly	Tyr	Phe	Thr	Gly		
		195					200					205					
tac	cta	atg	ggg	gac	ggg	gga	tca	gct	ctt	aac	tta	aac	ctt	att	tat		672
Tyr	Leu	Met	Gly	Asp	Gly	Gly	Ser	Ala	Leu	Asn	Leu	Asn	Leu	Ile	Tyr		
	210					215					220						
aac	ctt	gct	gac	ttt	gtt	aac	aag	att	cta	ttt	ggt	tta	att	ata	tgg		720
Asn	Leu	Ala	Asp	Phe	Val	Asn	Lys	Ile	Leu	Phe	Gly	Leu	Ile	Ile	Trp		
225					230					235					240		
aat	gtt	gct	gtt	aaa	gaa	tct	tct	aat	gct								750
Asn	Val	Ala	Val	Lys	Glu	Ser	Ser	Asn	Ala								
				245					250								

<210> 41

<211> 250

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 41

Met	Gly	Lys	Leu	Leu	Leu	Ile	Leu	Gly	Ser	Val	Ile	Ala	Leu	Pro	Thr	1	5	10	15
Phe	Ala	Ala	Gly	Gly	Gly	Asp	Leu	Asp	Ala	Ser	Asp	Tyr	Thr	Gly	Val	20	25	30	
Ser	Phe	Trp	Leu	Val	Thr	Ala	Ala	Leu	Leu	Ala	Ser	Thr	Val	Phe	Phe	35	40	45	
Phe	Val	Glu	Arg	Asp	Arg	Val	Ser	Ala	Lys	Trp	Lys	Thr	Ser	Leu	Thr	50	55	60	
Val	Ser	Gly	Leu	Val	Thr	Gly	Ile	Ala	Phe	Trp	His	Tyr	Met	Tyr	Met	65	70	75	80
Arg	Gly	Val	Trp	Ile	Glu	Thr	Gly	Asp	Ser	Pro	Thr	Val	Phe	Arg	Tyr	85	90	95	
Ile	Asp	Trp	Leu	Leu	Thr	Val	Pro	Leu	Leu	Ile	Cys	Glu	Phe	Tyr	Leu	100	105	110	
Ile	Leu	Ala	Ala	Ala	Thr	Asn	Val	Ala	Gly	Ser	Leu	Phe	Lys	Lys	Leu	115	120	125	
Leu	Val	Gly	Ser	Leu	Val	Met	Leu	Val	Phe	Gly	Tyr	Met	Gly	Glu	Ala	130	135	140	
Gly	Ile	Met	Ala	Ala	Trp	Pro	Ala	Phe	Ile	Ile	Gly	Cys	Leu	Ala	Trp	145	150	155	160
Val	Tyr	Met	Ile	Tyr	Glu	Leu	Tyr	Ala	Gly	Glu	Gly	Lys	Ser	Ala	Cys	165	170	175	
Asn	Thr	Ala	Ser	Pro	Ser	Val	Gln	Ser	Ala	Tyr	Asn	Thr	Met	Met	Ala	180	185	190	

Ile Ile Val Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
 195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
 210 215 220

Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
 225 230 235 240

Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 42

<211> 750

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(750)

<223> Proteorhodopsin variant from pcr clone MB100m7; GenBank #AF349992

<400> 42

atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca 48
 Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
 1 5 10 15

ttt gct gca ggt ggt ggt gac ctt gat gct agt gat tac act ggt gtt 96
 Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30

tct ttt tgg tta gtt act gct gct tta tta gca tct act gta ttt ttc 144
 Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45

ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act	192
Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr	
50 55 60	
gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tac atg	240
Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met	
65 70 75 80	
aga ggg gta tgg att gaa act ggt gat tcg cca act gta ttt aga tac	288
Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr	
85 90 95	
att gat tgg tta cta aca gtt cct cta tta ata tgt gaa ttc tac tta	336
Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu	
100 105 110	
att ctt gct gct gct act aat gtt gcc ggc tca tta ttt aag aaa ctt	384
Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu	
115 120 125	
cta gtt ggt tct ctt gtt atg ctt gtg ttt ggt tac atg ggt gaa gca	432
Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala	
130 135 140	
gga att atg gca gct tgg cct gca ttc att att ggg tgt tta gct tgg	480
Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp	
145 150 155 160	
gta tac atg att tat gaa cta tat gct gga gaa gga aaa tct gca tgt	528
Val Tyr Met Ile Tyr Glu Leu Tyr Ala Gly Glu Gly Lys Ser Ala Cys	
165 170 175	
aat act gca agt cct tcg gtt caa tca gct tac aac aca atg atg gct	576
Asn Thr Ala Ser Pro Ser Val Gln Ser Ala Tyr Asn Thr Met Met Ala	
180 185 190	
atc ata gtc ttc ggt tgg gca att tat cct gta ggt tat ttc aca ggt	624
Ile Ile Val Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly	
195 200 205	
tac cta atg ggt gac ggt gga tca gct ctt aac tta aac ctt att tat	672
Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr	
210 215 220	
aac ctt gct gac ttt gtt aac aag att cta ttt ggt tta att ata tgg	720
Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp	
225 230 235 240	

aat gct gct gtt aaa gaa tct tct aat gct
 Asn Ala Ala Val Lys Glu Ser Ser Asn Ala
 245 250

750

<210> 43

<211> 250

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 43

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
 1 5 10 15

Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30

Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
 65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
 85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
 100 105 110

Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu
 115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
130 135 140

Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp
145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Tyr Ala Gly Glu Gly Lys Ser Ala Cys
165 170 175

Asn Thr Ala Ser Pro Ser Val Gln Ser Ala Tyr Asn Thr Met Met Ala
180 185 190

Ile Ile Val Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
210 215 220

Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
225 230 235 240

Asn Ala Ala Val Lys Glu Ser Ser Asn Ala
245 250

<210> 44

<211> 750

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(750)

<223> Proteorhodopsin variant from pcr clone MB100m9; GenBank #AF349993

<400> 44

atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca 48
Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
1 5 10 15

ttt gct gca ggt ggt ggt gac ctt gat gct agt gat tac act ggt gtt 96
Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
20 25 30

tct ttt tgg tta gtt act gct gct tta tta gca tct act gta ttt ttc 144
Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
35 40 45

ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act 192
Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50 55 60

gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tat atg 240
Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
65 70 75 80

aga ggg gta tgg att gaa act ggt gat tcg cca act gta ttt aga tac 288
Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
85 90 95

ata gat tgg tta cta aca gtt cct tta tta ata tgt gaa ttc tac tta 336
Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
100 105 110

att ctt gcc gct gca act aat gtt gct gga tca tta ttt aag aaa tta 384
Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu
115 120 125

ctt gtt ggt tct ctt gtt atg ctt gtg ttt ggt tac atg ggt gaa gca 432
Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
130 135 140

gga atc atg gct gca tgg cct gca ttc att att ggg tgt tta gct tgg 480
Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp
145 150 155 160

gta tac atg att tat gaa cta tgg gct gga gaa gga aaa tct gca tgt 528

Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys
 165 170 175

aat act gca agt cct gct gtg caa tca gct tac aac aca atg atg tat 576
 Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr
 180 185 190

atc atc atc ttt ggt tgg gcg att tat cct gta ggt tat ttc aca ggt 624
 Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
 195 200 205

tac ctt atg ggt gac ggt gga tca gca ctt aac tta aac ctt att tat 672
 Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
 210 215 220

aac ctt gct gac ttt gtt aac aag att cta ttt ggt tta att ata tgg 720
 Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
 225 230 235 240

aat gtt gct gtt aaa gaa tct tct aat gct 750
 Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 45

<211> 250

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 45

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr
 1 5 10 15

Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val
 20 25 30

Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe
 35 40 45

Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50 55 60

Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met
65 70 75 80

Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr
85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Leu Ile Cys Glu Phe Tyr Leu
100 105 110

Ile Leu Ala Ala Ala Thr Asn Val Ala Gly Ser Leu Phe Lys Lys Leu
115 120 125

Leu Val Gly Ser Leu Val Met Leu Val Phe Gly Tyr Met Gly Glu Ala
130 135 140

Gly Ile Met Ala Ala Trp Pro Ala Phe Ile Ile Gly Cys Leu Ala Trp
145 150 155 160

Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys
165 170 175

Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr
180 185 190

Ile Ile Ile Phe Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
210 215 220

Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
225 230 235 240

Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 46

<211> 750

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(750)

<223> Proteorhodopsin variant from pcr clone MB100m10; GenBank #AF34999

<400> 46

atg ggt aaa tta tta ctg ata tta ggt agt gtt att gca ctt cct aca	48
Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Val Ile Ala Leu Pro Thr	
1 5 10 15	

ttt gct gca ggt ggc ggt gac ctt gat gct agt gat tac act ggt gtt	96
Phe Ala Ala Gly Gly Gly Asp Leu Asp Ala Ser Asp Tyr Thr Gly Val	
20 25 30	

tct ttt tgg tta gtt aca gct gct cta tta gcg tct act gta ttt ttc	144
Ser Phe Trp Leu Val Thr Ala Ala Leu Leu Ala Ser Thr Val Phe Phe	
35 40 45	

ttt gtt gaa aga gat aga gtt tct gca aaa tgg aaa aca tca tta act	192
Phe Val Glu Arg Asp Arg Val Ser Ala Lys Trp Lys Thr Ser Leu Thr	
50 55 60	

gta tct ggt ctt gtt act ggt att gct ttc tgg cat tac atg tat atg	240
Val Ser Gly Leu Val Thr Gly Ile Ala Phe Trp His Tyr Met Tyr Met	
65 70 75 80	

aga gga gta tgg att gaa act ggt gat tcg cca act gta ttt aga tac	288
Arg Gly Val Trp Ile Glu Thr Gly Asp Ser Pro Thr Val Phe Arg Tyr	

85										90					95					
att	gat	tgg	tta	cta	aca	gtt	cct	tta	tta	ata	tgt	gaa	ttc	tac	tta		336			
Ile	Asp	Trp	Leu	Leu	Thr	Val	Pro	Leu	Leu	Ile	Cys	Glu	Phe	Tyr	Leu					
			100					105					110							
att	ctt	gct	gct	gca	act	aat	gtt	gcc	ggc	tca	tta	ttt	aag	aaa	ctt		384			
Ile	Leu	Ala	Ala	Ala	Thr	Asn	Val	Ala	Gly	Ser	Leu	Phe	Lys	Lys	Leu					
		115					120					125								
cta	gtt	ggg	tct	ctt	gtt	atg	ctt	gtg	ttt	ggg	tac	atg	ggg	gaa	gca		432			
Leu	Val	Gly	Ser	Leu	Val	Met	Leu	Val	Phe	Gly	Tyr	Met	Gly	Glu	Ala					
	130					135					140									
gga	ata	atg	gcg	gct	tgg	cct	gca	ttc	atc	gtt	gga	tgt	tta	gca	tgg		480			
Gly	Ile	Met	Ala	Ala	Trp	Pro	Ala	Phe	Ile	Val	Gly	Cys	Leu	Ala	Trp					
145					150					155					160					
gta	tat	atg	att	tat	gaa	cta	tgg	gct	ggg	gaa	gga	aaa	tct	gca	tgt		528			
Val	Tyr	Met	Ile	Tyr	Glu	Leu	Trp	Ala	Gly	Glu	Gly	Lys	Ser	Ala	Cys					
				165					170					175						
aat	act	gca	agt	cct	gct	gta	cag	tca	gct	tac	aac	aca	atg	atg	tat		576			
Asn	Thr	Ala	Ser	Pro	Ala	Val	Gln	Ser	Ala	Tyr	Asn	Thr	Met	Met	Tyr					
			180					185					190							
atc	atc	atc	gtt	ggg	tgg	gca	att	tat	cct	gta	ggg	tat	ttc	aca	ggg		624			
Ile	Ile	Ile	Val	Gly	Trp	Ala	Ile	Tyr	Pro	Val	Gly	Tyr	Phe	Thr	Gly					
		195				200						205								
tac	cta	atg	ggg	gac	ggg	gga	tca	gct	ctt	aat	cta	aac	ctt	att	tat		672			
Tyr	Leu	Met	Gly	Asp	Gly	Gly	Ser	Ala	Leu	Asn	Leu	Asn	Leu	Ile	Tyr					
	210					215					220									
aac	ctt	gct	gac	ttt	gtt	aac	aag	att	cta	ttt	ggg	tta	att	ata	tgg		720			
Asn	Leu	Ala	Asp	Phe	Val	Asn	Lys	Ile	Leu	Phe	Gly	Leu	Ile	Ile	Trp					
225					230					235					240					
aat	gtt	gct	gtt	aaa	gaa	tct	tct	aat	gct								750			
Asn	Val	Ala	Val	Lys	Glu	Ser	Ser	Asn	Ala											
				245				250												

<210> 47

<211> 250

Val Tyr Met Ile Tyr Glu Leu Trp Ala Gly Glu Gly Lys Ser Ala Cys
 165 170 175

Asn Thr Ala Ser Pro Ala Val Gln Ser Ala Tyr Asn Thr Met Met Tyr
 180 185 190

Ile Ile Ile Val Gly Trp Ala Ile Tyr Pro Val Gly Tyr Phe Thr Gly
 195 200 205

Tyr Leu Met Gly Asp Gly Gly Ser Ala Leu Asn Leu Asn Leu Ile Tyr
 210 215 220

Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile Trp
 225 230 235 240

Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 48

<211> 753

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(753)

<223> Proteorhodopsin variant from pcr clone PALB1; GenBank #AF349995

<400> 48

atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca
 Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
 1 5 10 15

48

ttt	gct	gct	gct	ggt	ggc	gat	cta	gat	ata	agt	gat	act	gtt	ggt	ggt		96
Phe	Ala	Ala	Ala	Gly	Gly	Asp	Leu	Asp	Ile	Ser	Asp	Thr	Val	Gly	Val		
			20					25					30				
tca	ttc	tgg	ctg	gtt	aca	gct	ggt	atg	tta	gcg	gca	act	gta	ttc	ttt		144
Ser	Phe	Trp	Leu	Val	Thr	Ala	Gly	Met	Leu	Ala	Ala	Thr	Val	Phe	Phe		
		35					40					45					
ttt	gta	gaa	aga	gac	caa	gtc	agc	gct	aag	tgg	aaa	act	tca	ctt	act		192
Phe	Val	Glu	Arg	Asp	Gln	Val	Ser	Ala	Lys	Trp	Lys	Thr	Ser	Leu	Thr		
	50					55					60						
gta	tct	ggt	tta	att	act	ggt	ata	gct	ttt	tgg	cat	tat	ctc	tac	atg		240
Val	Ser	Gly	Leu	Ile	Thr	Gly	Ile	Ala	Phe	Trp	His	Tyr	Leu	Tyr	Met		
65					70					75					80		
aga	ggt	gtt	tgg	ata	gat	act	ggt	gat	aca	cca	aca	gta	ttt	aga	tat		288
Arg	Gly	Val	Trp	Ile	Asp	Thr	Gly	Asp	Thr	Pro	Thr	Val	Phe	Arg	Tyr		
				85					90					95			
att	gat	tgg	cta	tta	act	gtt	cca	tta	caa	atg	gtt	gag	ttc	tat	cta		336
Ile	Asp	Trp	Leu	Leu	Thr	Val	Pro	Leu	Gln	Met	Val	Glu	Phe	Tyr	Leu		
			100					105					110				
att	ctt	gct	gct	tgt	aca	agt	gtt	gct	gct	tca	tta	ttt	aag	aag	ctt		384
Ile	Leu	Ala	Ala	Cys	Thr	Ser	Val	Ala	Ala	Ser	Leu	Phe	Lys	Lys	Leu		
		115					120					125					
cta	gct	ggt	tca	tta	gta	atg	tta	ggt	gct	gga	ttt	gca	ggc	gaa	gct		432
Leu	Ala	Gly	Ser	Leu	Val	Met	Leu	Gly	Ala	Gly	Phe	Ala	Gly	Glu	Ala		
	130					135					140						
ggt	tta	gct	cct	gta	tta	cct	gct	ttc	att	ctt	ggt	atg	gct	ggt	tgg		480
Gly	Leu	Ala	Pro	Val	Leu	Pro	Ala	Phe	Ile	Leu	Gly	Met	Ala	Gly	Trp		
145					150					155					160		
tta	tac	atg	att	tat	gag	cta	cat	atg	ggt	gaa	ggt	aag	gct	gct	gta		528
Leu	Tyr	Met	Ile	Tyr	Glu	Leu	His	Met	Gly	Glu	Gly	Lys	Ala	Ala	Val		
				165				170						175			
agt	act	gca	agt	cct	gct	gtt	aac	tct	gct	tac	aat	gca	atg	atg	aag		576
Ser	Thr	Ala	Ser	Pro	Ala	Val	Asn	Ser	Ala	Tyr	Asn	Ala	Met	Met	Lys		
			180					185					190				
att	att	gtt	att	gga	tgg	gca	att	tat	cct	gct	gga	tat	gct	gct	ggt		624
Ile	Ile	Val	Ile	Gly	Trp	Ala	Ile	Tyr	Pro	Ala	Gly	Tyr	Ala	Ala	Gly		
		195					200					205					

tac cta atg agt ggt gac ggt gta tac gct tca aac tta aac ctt ata 672
Tyr Leu Met Ser Gly Asp Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
210 215 220

tat aac ctt gct gac ttt gtt aac aag att cta ttt ggt ttg atc att 720
Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
225 230 235 240

tgg aat gtt gct gtt aaa gaa tct tct aat gct 753
Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
245 250

<210> 49

<211> 251

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 49

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
1 5 10 15

Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
20 25 30

Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
35 40 45

Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50 55 60

Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
65 70 75 80

Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
85 90 95

100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250

Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
100 105 110

Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu
115 120 125

Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
130 135 140

Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Leu Gly Met Ala Gly Trp
145 150 155 160

Leu Tyr Met Ile Tyr Glu Leu His Met Gly Glu Gly Lys Ala Ala Val
165 170 175

Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Lys
180 185 190

Ile Ile Val Ile Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
195 200 205

Tyr Leu Met Ser Gly Asp Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
210 215 220

Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
225 230 235 240

Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
245 250

<210> 50

<211> 753

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(753)

<223> Proteorhodopsin variant from pcr clone PALB2; GenBank #AF349996

<400> 50

atg	ggt	aaa	tta	tta	ctg	ata	tta	ggt	agt	gct	att	gca	ctt	cca	tca	48
Met	Gly	Lys	Leu	Leu	Leu	Ile	Leu	Gly	Ser	Ala	Ile	Ala	Leu	Pro	Ser	
1			5					10					15			

ttt	gct	gct	gct	ggt	ggc	gat	cta	gat	ata	agt	gat	act	ggt	ggt	ggt	96
Phe	Ala	Ala	Ala	Gly	Gly	Asp	Leu	Asp	Ile	Ser	Asp	Thr	Val	Gly	Val	
			20					25					30			

tca	ttc	tgg	ctg	gtt	aca	gct	ggt	atg	tta	gcg	gca	act	gtg	ttc	ttt	144
Ser	Phe	Trp	Leu	Val	Thr	Ala	Gly	Met	Leu	Ala	Ala	Thr	Val	Phe	Phe	
		35					40					45				

ttt	gta	gaa	aga	gac	caa	gtc	agc	gct	gag	tgg	aaa	act	tca	ctt	act	192
Phe	Val	Glu	Arg	Asp	Gln	Val	Ser	Ala	Glu	Trp	Lys	Thr	Ser	Leu	Thr	
	50					55					60					

gta	tct	ggt	tta	att	act	ggt	ata	gct	ttt	tgg	cat	tat	ctc	tat	atg	240
Val	Ser	Gly	Leu	Ile	Thr	Gly	Ile	Ala	Phe	Trp	His	Tyr	Leu	Tyr	Met	
65					70				75					80		

aga	ggt	gtt	tgg	ata	gat	act	ggt	gat	acc	cca	aca	gta	ttc	aga	tat	288
Arg	Gly	Val	Trp	Ile	Asp	Thr	Gly	Asp	Thr	Pro	Thr	Val	Phe	Arg	Tyr	
				85				90						95		

att	gat	tgg	tta	tta	act	gtt	cca	tta	caa	atg	gtt	gag	ttc	tat	cta	336
Ile	Asp	Trp	Leu	Leu	Thr	Val	Pro	Leu	Gln	Met	Val	Glu	Phe	Tyr	Leu	
			100					105					110			

att	ctt	gct	gct	tgt	aca	agt	gtt	gct	gct	tca	tta	ttt	aag	aag	ctt	384
Ile	Leu	Ala	Ala	Cys	Thr	Ser	Val	Ala	Ala	Ser	Leu	Phe	Lys	Lys	Leu	
		115					120					125				

cta	gct	ggt	tca	tta	gta	atg	tta	ggt	gct	gga	ttt	gca	ggc	gaa	gct	432
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
 210 215 220

Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
 225 230 235 240

Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 52

<211> 753

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(753)

<223> Proteorhodopsin variant from pcr clone PALB5; GenBank#AF349997

<400> 52

atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca	48
Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser	
1 5 10 15	

ttt gct gct gct ggt ggc gat cta gat ata agt gat act gtt ggt gtt	96
Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val	
20 25 30	

tca ttc tgg ctg gtt aca gct ggt atg tta gcg gca act gtg ttc ttt	144
Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe	
35 40 45	

ttt gta gaa aga gac caa gtc agc gct aag tgg aaa act tca ctt act	192
Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr	
50 55 60	

gta tct ggt tta att act ggt ata gcc ttt tgg cat tat ctc tat atg	240
Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met	
65 70 75 80	
aga ggt gtt tgg ata gac act ggt gat acc cca aca gta ttc aga tat	288
Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr	
85 90 95	
att gat tgg tta tta act gtt cca tta caa atg gtt gag ttc tat cta	336
Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu	
100 105 110	
att ctt gct gct tgt aca aat gtt gct gct tca tta ttt aag aag ctt	384
Ile Leu Ala Ala Cys Thr Asn Val Ala Ala Ser Leu Phe Lys Lys Leu	
115 120 125	
cta gct ggt tca tta gta atg tta ggt gct gga ttt gca ggc gaa gct	432
Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala	
130 135 140	
gga tta gct cct gta tgg cct gct ttc att att ggt atg gct gga tgg	480
Gly Leu Ala Pro Val Trp Pro Ala Phe Ile Ile Gly Met Ala Gly Trp	
145 150 155 160	
tta tac atg att tat gag cta tat atg ggt gaa ggt aag gct gct gta	528
Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val	
165 170 175	
agt act gca agt cct gct gtt aac tct gca tac aac gca atg atg atg	576
Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Met	
180 185 190	
att att gtt gtt gga tgg gca att tat cct gct gga tat gct gct ggt	624
Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly	
195 200 205	
tac cta atg ggt ggc gaa ggt gta tac gct tca aac cta aac ctt ata	672
Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile	
210 215 220	
tat aac ctt gct gac ttt gtt aac aag att cta ttt ggt ttg atc att	720
Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile	
225 230 235 240	
tgg aat gtt gct gtt aaa gaa tct tct aat gct	753
Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala	
245 250	

<210> 53

<211> 251

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 53

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
1 5 10 15

Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
20 25 30

Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
35 40 45

Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50 55 60

Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
65 70 75 80

Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
100 105 110

Ile Leu Ala Ala Cys Thr Asn Val Ala Ala Ser Leu Phe Lys Lys Leu
115 120 125

Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
130 135 140

Gly Leu Ala Pro Val Trp Pro Ala Phe Ile Ile Gly Met Ala Gly Trp
 145 150 155 160

Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val
 165 170 175

Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Met
 180 185 190

Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
 195 200 205

Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
 210 215 220

Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
 225 230 235 240

Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 54

<211> 753

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(753)

<223> Proteorhodopsin variant from pcr clone PalB7; GenBank #AF349999

Parameter	Value	Unit
Initial concentration	1.0	g/L
Initial pH	7.0	
Temperature	25	°C
Time	0, 1, 2, 4, 8, 16, 32, 64, 128, 256, 512, 1024, 2048, 4096, 8192, 16384, 32768, 65536, 131072, 262144, 524288, 1048576, 2097152, 4194304, 8388608, 16777216, 33554432, 67108864, 134217728, 268435456, 536870912, 1073741824, 2147483648, 4294967296, 8589934592, 17179869184, 34359738368, 68719476736, 137438953472, 274877906944, 549755813888, 1099511627776, 2199023255552, 4398046511104, 8796093022208, 17592186044416, 35184372088832, 70368744177664, 140737488355328, 281474976710656, 562949953421312, 1125899906842624, 2251799813685248, 4503599627370496, 9007199254740992, 18014398509481984, 36028797018963968, 72057594037927936, 144115188075855872, 288230376151711744, 576460752303423488, 1152921504606846976, 2305843009213693952, 4611686018427387904, 9223372036854775808, 18446744073709551616, 36893488147419103232, 73786976294838206464, 147573952589676412928, 295147905179352825856, 590295810358705651712, 1180591620717411303424, 2361183241434822606848, 4722366482869645213696, 9444732965739290427392, 18889465931478580854784, 37778931862957161709568, 75557863725914323419136, 151115727451828646838272, 302231454903657293676544, 604462909807314587353088, 1208925819614629174706176, 2417851639229258349412352, 4835703278458516698824704, 9671406556917033397649408, 19342813113834066795298816, 38685626227668133590597632, 77371252455336267181195264, 154742504910672534362390528, 309485009821345068724781056, 618970019642690137449562112, 1237940039285380274899124224, 2475880078570760549798248448, 4951760157141521099596496896, 9903520314283042199192993792, 19807040628566084398385987584, 39614081257132168796771975168, 79228162514264337593543950336, 158456325028528675187087900672, 316912650057057350374175801344, 633825300114114700748351602688, 1267650600228229401496703205376, 2535301200456458802993406410752, 5070602400912917605986812821504, 10141204801825835211973625643008, 20282409603651670423947251286016, 40564819207303340847894502572032, 81129638414606681695789005144064, 162259276829213363391578010288128, 324518553658426726783156020576256, 649037107316853453566312041152512, 1298074214633706907132624082305024, 2596148429267413814265248164610048, 5192296858534827628530496329220096, 10384593717069655257060992658440192, 20769187434139310514121985316880384, 41538374868278621028243970633760768, 83076749736557242056487941267521536, 166153499473114484112975882535043072, 332306998946228968225951765070086144, 664613997892457936451903530140172288, 1329227995784915872903807060280344576, 2658455991569831745807614120560689152, 5316911983139663491615228241121378304, 10633823966279326983230456482242756608, 21267647932558653966460912964485513216, 42535295865117307932921825928971026432, 85070591730234615865843651857942052864, 170141183460469231731687303715884105728, 340282366920938463463374607431768211456, 680564733841876926926749214863536422912, 1361129467683753853853498429727072845824, 2722258935367507707706996859454145691648, 5444517870735015415413993718908291383296, 10889035741470030830827987437816582766592, 21778071482940061661655974875633165533184, 43556142965880123323311949751266331066368, 87112285931760246646623899502532662132736, 174224571863520493293247799005065324265472, 348449143727040986586495598010130648530944, 696898287454081973172991196020261297061888, 1393796574908163946345982392040522594123776, 2787593149816327892691964784081045188247552, 5575186299632655785383929568162090376495104, 11150372599265311570767859136324180752990208, 22300745198530623141535718272648361505980416, 44601490397061246283071436545296723011960832, 89202980794122492566142873090593446023921664, 178405961588244985132285746181186892047843328, 356811923176489970264571492362373784095686656, 713623846352979940529142984724747568191373312, 1427247692705959881058285969449495136382746624, 2854495385411919762116571938898990272765493248, 5708990770823839524233143877797980545530986496, 11417981541647679048466287755595961091061972992, 2283596308329	

atg Met 1	ggg Gly	aaa Lys	tta Leu	tta Leu 5	ctg Leu	ata Ile	tta Leu	ggg Gly	agt Ser 10	gct Ala	att Ile	gcg Ala	ctt Leu	cca Pro 15	tca Ser	48
ttt Phe	gct Ala	gct Ala	gct Ala 20	ggg Gly	ggc Gly	gat Asp	cta Leu	gat Asp 25	ata Ile	agt Ser	gat Asp	act Thr	gtt Val 30	ggg Gly	gtt Val	96
tca Ser	ttc Phe	tgg Trp 35	ctg Leu	gtt Val	acg Thr	gct Ala	ggg Gly 40	atg Met	tta Leu	gcg Ala	gca Ala	act Thr 45	gta Val	ttc Phe	ttt Phe	144
ttt Phe 50	gta Val	gaa Glu	aga Arg	gac Asp	caa Gln	gtc Val 55	agc Ser	gct Ala	aag Lys	tgg Trp	aaa Lys 60	act Thr	tca Ser	ctt Leu	act Thr	192
gta Val 65	tct Ser	ggg Gly	tta Leu	att Ile	act Thr 70	ggg Gly	ata Ile	gct Ala	ttt Phe	tgg Trp 75	cat His	tat Tyr	ctc Leu	tac Tyr	atg Met 80	240
aga Arg	ggg Gly	gtt Val	tgg Trp	ata Ile 85	gat Asp	act Thr	ggg Gly	gat Asp	aca Thr 90	cca Pro	aca Thr	gta Val	ttt Phe	aga Arg 95	tat Tyr	288
att Ile	gat Asp	tgg Trp	tta Leu 100	tta Leu	act Thr	gtt Val	cca Pro	tta Leu 105	caa Gln	atg Met	gtt Val	gag Glu	ttc Phe 110	tat Tyr	cta Leu	336
att Ile	ctt Leu	gcc Ala 115	gct Ala	tgt Cys	aca Thr	agt Ser	gtt Val 120	gct Ala	gct Ala	tca Ser	tta Leu	ttt Phe 125	aag Lys	aag Lys	ctt Leu	384
cta Leu	gct Ala 130	ggg Gly	tca Ser	ttg Leu	gta Val	atg Met 135	tta Leu	ggg Gly	gct Ala	gga Gly	tct Ser 140	gca Ala	ggc Gly	gaa Glu	gct Ala	432
gga Gly 145	tta Leu	gct Ala	cct Pro	gta Val 150	tta Leu	cct Pro	gct Ala	ttc Phe	att Ile 155	att Ile	ggg Gly	atg Met	gct Ala	gga Gly	tgg Trp 160	480
tta Leu	tac Tyr	atg Met	att Ile	tat Tyr 165	gag Glu	cta Leu	tat Tyr	atg Met	ggg Gly 170	gaa Glu	ggg Gly	aag Lys	gct Ala	gct Ala	gta Val 175	528
agt Met	act Thr	gca Ala	agt Thr	cct Leu	gct Val	gtt Ile	aac Gln	tct Leu	gca Ala	tac Ser	aac Thr	gca Ala	atg Thr	atg Thr	atg Thr	576

Ser	Thr	Ala	Ser	Pro	Ala	Val	Asn	Ser	Ala	Tyr	Asn	Ala	Met	Met	Met	
			180					185					190			
att	att	gtt	gtt	gga	tgg	gca	att	tat	cct	gct	gga	tat	gct	gct	ggt	624
Ile	Ile	Val	Val	Gly	Trp	Ala	Ile	Tyr	Pro	Ala	Gly	Tyr	Ala	Ala	Gly	
		195					200					205				
tac	cta	atg	ggt	ggc	gaa	ggt	gta	tac	gct	tca	aac	tta	aac	ctc	ata	672
Tyr	Leu	Met	Gly	Gly	Glu	Gly	Val	Tyr	Ala	Ser	Asn	Leu	Asn	Leu	Ile	
	210					215					220					
tat	aac	ctt	gct	gac	ttt	gtt	aac	aag	att	cta	ttt	ggt	ttg	atc	att	720
Tyr	Asn	Leu	Ala	Asp	Phe	Val	Asn	Lys	Ile	Leu	Phe	Gly	Leu	Ile	Ile	
225					230					235					240	
tgg	aat	gtt	gct	gtt	aaa	gaa	tct	tct	aat	gct						753
Trp	Asn	Val	Ala	Val	Lys	Glu	Ser	Ser	Asn	Ala						
				245					250							

<210> 55

<211> 251

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 55

Met	Gly	Lys	Leu	Leu	Leu	Ile	Leu	Gly	Ser	Ala	Ile	Ala	Leu	Pro	Ser
1				5					10					15	
Phe	Ala	Ala	Ala	Gly	Gly	Asp	Leu	Asp	Ile	Ser	Asp	Thr	Val	Gly	Val
			20					25					30		
Ser	Phe	Trp	Leu	Val	Thr	Ala	Gly	Met	Leu	Ala	Ala	Thr	Val	Phe	Phe
		35					40					45			
Phe	Val	Glu	Arg	Asp	Gln	Val	Ser	Ala	Lys	Trp	Lys	Thr	Ser	Leu	Thr
	50					55					60				

Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
65 70 75 80

Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
100 105 110

Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu
115 120 125

Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Ser Ala Gly Glu Ala
130 135 140

Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp
145 150 155 160

Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val
165 170 175

Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Met
180 185 190

Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
195 200 205

Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
210 215 220

Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
225 230 235 240

Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
245 250

<210> 56
 <211> 753
 <212> DNA
 <213> Naturally occurring gamma proteobacterium

 <220>
 <221> CDS
 <222> (1)..(753)
 <223> Proteorhodopsin variant from pcr clone PalB6; GenBank # AF349998

<400> 56
 atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca 48
 Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
 1 5 10 15

 ttt gct gct gct ggt ggc gat cta gat ata agt gat act gtt ggt gtt 96
 Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
 20 25 30

 tca ttc tgg ctg gtt aca gct ggt atg tta gcg gca act gtg ttc ttt 144
 Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
 35 40 45

 ttt gta gaa aga gac caa gtc agc gct aag tgg aaa act tca ctt act 192
 Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60

 gta tct ggt tta att act ggt ata gct ttt tgg cat tat ctc tat atg 240
 Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
 65 70 75 80

 aga ggt gtt tgg ata gac act ggt gat acc cca aca gta ttc aga tat 288
 Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
 85 90 95

 att gat tgg tta tta act gtt cca tta caa atg gtt gag ttc tat cta 336
 Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu

	100	105	110	
	att ctt gct gct tgt aca aat gtt gct gct tca tta ttt aag aag ctt			384
	Ile Leu Ala Ala Cys Thr Asn Val Ala Ala Ser Leu Phe Lys Lys Leu			
	115	120	125	
	cta gct ggt tca tta gta atg tta ggt gct gga ttt gca ggc gaa gct			432
	Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala			
	130	135	140	
	gga tta gct cct gta tgg cct gct ttc att att ggt atg gct gga tgg			480
	Gly Leu Ala Pro Val Trp Pro Ala Phe Ile Ile Gly Met Ala Gly Trp			
	145	150	155	160
	tta tac atg att tat gag cta tat atg ggt gaa ggt aag gct gct gta			528
	Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val			
		165	170	175
	agt act gca agt cct gct gtt aac tct gca tac aac gca atg atg gtg			576
	Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Val			
		180	185	190
	att att gtt gtt gga tgg gca att tat cct gct gga tat gct gct ggt			624
	Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly			
		195	200	205
	tac cta atg ggt ggc gaa ggt gta tac gct tca aac cta aac ctt ata			672
	Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile			
		210	215	220
	tat aac ctt gct gac ttt gtt aac aag att cta ttt ggt ttg atc att			720
	Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile			
	225	230	235	240
	tgg aat gtt gct gtt aaa gaa tct tct aat gct			753
	Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala			
		245	250	

<210> 57

<211> 251

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 57

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
1 5 10 15

Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
20 25 30

Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
35 40 45

Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50 55 60

Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
65 70 75 80

Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
100 105 110

Ile Leu Ala Ala Cys Thr Asn Val Ala Ala Ser Leu Phe Lys Lys Leu
115 120 125

Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
130 135 140

Gly Leu Ala Pro Val Trp Pro Ala Phe Ile Ile Gly Met Ala Gly Trp
145 150 155 160

Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val
165 170 175

Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Val
180 185 190

Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
195 200 205

Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
210 215 220

Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
225 230 235 240

Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
245 250

<210> 58

<211> 753

<212> DNA

<213> Naturally occurring gamma proteobacteria

<220>

<221> CDS

<222> (1)..(753)

<223> Proteorhodopsin variant from pcr clone PalB8; GenBank #AF350000

<400> 58

atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca	48
Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser	
1 5 10 15	

ttt gct gct gct ggt ggc gat cta gat ata agt gat act gtt ggt gtt	96
Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val	
20 25 30	

tca	ttc	tgg	ctg	gtt	aca	gct	ggg	atg	tta	gcg	gca	act	gtg	ttc	ttt	144
Ser	Phe		Leu	Val	Thr	Ala	Gly	Met	Leu	Ala	Ala	Thr	Val	Phe	Phe	
	35						40					45				
ttt	gta	gaa	aga	gac	caa	gtc	agc	gct	aag	tgg	aaa	act	tca	ctt	act	192
Phe	Val	Glu	Arg	Asp	Gln	Val	Ser	Ala	Lys	Trp	Lys	Thr	Ser	Leu	Thr	
	50					55					60					
gta	tct	ggg	tta	att	act	ggg	ata	gct	ttt	tgg	cat	tat	ctc	tat	atg	240
Val	Ser	Gly	Leu	Ile	Thr	Gly	Ile	Ala	Phe	Trp	His	Tyr	Leu	Tyr	Met	
65					70					75					80	
aga	ggg	gtt	tgg	ata	gac	act	ggg	gat	acc	cca	aca	gta	ttc	aga	tat	288
Arg	Gly	Val	Trp	Ile	Asp	Thr	Gly	Asp	Thr	Pro	Thr	Val	Phe	Arg	Tyr	
				85					90					95		
att	gat	tgg	tta	tta	act	gtt	cca	tta	caa	atg	gtt	gag	ttc	tat	cta	336
Ile	Asp	Trp	Leu	Leu	Thr	Val	Pro	Leu	Gln	Met	Val	Glu	Phe	Tyr	Leu	
			100					105					110			
att	ctt	gct	gct	tgt	aca	agt	gtt	gct	gct	tca	tta	ttt	aag	aag	ctt	384
Ile	Leu	Ala	Ala	Cys	Thr	Ser	Val	Ala	Ala	Ser	Leu	Phe	Lys	Lys	Leu	
		115					120					125				
cta	gct	ggg	tca	tta	gta	atg	tta	ggg	gct	gga	ttt	gca	ggc	gaa	gct	432
Leu	Ala	Gly	Ser	Leu	Val	Met	Leu	Gly	Ala	Gly	Phe	Ala	Gly	Glu	Ala	
	130					135					140					
gga	tta	gct	cct	gta	tta	cct	gct	ttc	att	att	ggg	atg	gct	gga	tgg	480
Gly	Leu	Ala	Pro	Val	Leu	Pro	Ala	Phe	Ile	Ile	Gly	Met	Ala	Gly	Trp	
145					150					155					160	
tta	tac	atg	att	tat	gag	cta	tat	atg	ggg	gaa	ggg	aag	gct	gct	gta	528
Leu	Tyr	Met	Ile	Tyr	Glu	Leu	Tyr	Met	Gly	Glu	Gly	Lys	Ala	Ala	Val	
				165					170					175		
agt	act	gca	agt	cct	gct	gtt	aac	tct	gca	tac	aac	gca	atg	atg	atg	576
Ser	Thr	Ala	Ser	Pro	Ala	Val	Asn	Ser	Ala	Tyr	Asn	Ala	Met	Met	Met	
			180					185					190			
att	att	gtt	gtt	gga	tgg	gca	att	tat	cct	gct	gga	tat	gct	gct	ggg	624
Ile	Ile	Val	Val	Gly	Trp	Ala	Ile	Tyr	Pro	Ala	Gly	Tyr	Ala	Ala	Gly	
		195					200					205				
tac	cta	atg	ggg	ggc	gaa	ggg	gta	tac	gct	tca	aac	tta	aac	ctt	ata	672
Tyr	Leu	Met	Gly	Gly	Glu	Gly	Val	Tyr	Ala	Ser	Asn	Leu	Asn	Leu	Ile	
	210					215					220					

[illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible]

Gly	Leu	Ala	Pro	Val	Leu	Pro	Ala	Phe	Ile	Ile	Gly	Met	Ala	Gly	Trp	
145					150					155					160	
tta	tac	atg	att	tat	gag	cta	tat	atg	ggg	gaa	ggc	aag	gct	gct	gta	528
Leu	Tyr	Met	Ile	Tyr	Glu	Leu	Tyr	Met	Gly	Glu	Gly	Lys	Ala	Ala	Val	
				165					170					175		
agt	act	gca	agt	cct	gct	gtt	aac	cct	gca	tac	aac	gca	atg	atg	atg	576
Ser	Thr	Ala	Ser	Pro	Ala	Val	Asn	Pro	Ala	Tyr	Asn	Ala	Met	Met	Met	
			180				185						190			
att	att	gtt	gtt	gga	tgg	gca	att	tat	cct	gct	gga	tat	gct	gct	ggg	624
Ile	Ile	Val	Val	Gly	Trp	Ala	Ile	Tyr	Pro	Ala	Gly	Tyr	Ala	Ala	Gly	
		195					200					205				
tac	cta	atg	ggg	ggc	gaa	ggg	gta	tac	gct	tca	aac	tta	aac	ctt	ata	672
Tyr	Leu	Met	Gly	Gly	Glu	Gly	Val	Tyr	Ala	Ser	Asn	Leu	Asn	Leu	Ile	
	210					215					220					
tat	aac	ctt	gct	gac	ttt	gtt	aac	aag	att	cta	ttt	ggg	ttg	atc	att	720
Tyr	Asn	Leu	Ala	Asp	Phe	Val	Asn	Lys	Ile	Leu	Phe	Gly	Leu	Ile	Ile	
225					230					235					240	
tgg	aat	gtt	gct	gtt	aaa	gaa	tct	tct	aat	gct						753
Trp	Asn	Val	Ala	Val	Lys	Glu	Ser	Ser	Asn	Ala						
				245					250							
<210>	61															
<211>	251															
<212>	PRT															
<213>	Naturally occurring gamma proteobacteria															
<400>	61															
Met	Gly	Lys	Leu	Leu	Leu	Ile	Leu	Gly	Ser	Ala	Ile	Ala	Leu	Pro	Ser	
1				5					10					15		
Phe	Ala	Ala	Ala	Gly	Gly	Asp	Leu	Asp	Ile	Ser	Asp	Thr	Val	Gly	Val	
			20					25					30			

Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
35 40 45

Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50 55 60

Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
65 70 75 80

Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Val Val Glu Phe Tyr Leu
100 105 110

Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu
115 120 125

Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
130 135 140

Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp
145 150 155 160

Leu Tyr Met Ile Tyr Glu Leu Tyr Met Gly Glu Gly Lys Ala Ala Val
165 170 175

Ser Thr Ala Ser Pro Ala Val Asn Pro Ala Tyr Asn Ala Met Met Met
180 185 190

Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
195 200 205

Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
210 215 220

aga	ggt	ggt	tgg	ata	gat	act	ggt	gat	aca	cca	aca	gta	ttt	aga	tat	288
Arg	Gly	Val	Trp	Ile	Asp	Thr	Gly	Asp	Thr	Pro	Thr	Val	Phe	Arg	Tyr	
				85					90					95		
att	gat	tgg	tta	tta	act	ggt	cca	tta	caa	atg	ggt	gag	ttc	tat	cta	336
Ile	Asp	Trp	Leu	Leu	Thr	Val	Pro	Leu	Gln	Met	Val	Glu	Phe	Tyr	Leu	
				100					105					110		
att	ctt	gct	gct	tgt	aca	agt	ggt	gct	gct	tca	tta	ttt	aag	aag	ctt	384
Ile	Leu	Ala	Ala	Cys	Thr	Ser	Val	Ala	Ala	Ser	Leu	Phe	Lys	Lys	Leu	
				115					120					125		
cta	gct	ggt	tca	tta	gta	atg	tta	ggt	gct	gga	ttt	gca	ggc	gaa	gct	432
Leu	Ala	Gly	Ser	Leu	Val	Met	Leu	Gly	Ala	Gly	Phe	Ala	Gly	Glu	Ala	
				130					135					140		
ggt	tta	gct	cct	gta	tta	cct	gct	ttc	att	att	ggt	atg	gct	gga	tgg	480
Gly	Leu	Ala	Pro	Val	Leu	Pro	Ala	Phe	Ile	Ile	Gly	Met	Ala	Gly	Trp	
				145					150					155		
tta	tac	atg	att	tat	gag	cta	cat	atg	ggt	gaa	ggt	aag	gct	gct	gta	528
Leu	Tyr	Met	Ile	Tyr	Glu	Leu	His	Met	Gly	Glu	Gly	Lys	Ala	Ala	Val	
				165					170					175		
agt	act	gca	agt	cct	gct	ggt	aac	tct	gca	tac	aac	gca	atg	atg	aag	576
Ser	Thr	Ala	Ser	Pro	Ala	Val	Asn	Ser	Ala	Tyr	Asn	Ala	Met	Met	Lys	
				180					185					190		
att	att	ggt	att	gga	tgg	gca	att	tat	cct	gct	gga	tat	gct	gct	ggt	624
Ile	Ile	Val	Ile	Gly	Trp	Ala	Ile	Tyr	Pro	Ala	Gly	Tyr	Ala	Ala	Gly	
				195					200					205		
tac	cta	atg	agt	ggt	gac	ggt	gta	tac	gct	tca	aac	tta	aac	ctt	ata	672
Tyr	Leu	Met	Ser	Gly	Asp	Gly	Val	Tyr	Ala	Ser	Asn	Leu	Asn	Leu	Ile	
				210					215					220		
tat	aac	ctt	gct	gac	ttt	ggt	aac	aag	att	cta	ttt	ggt	ttg	atc	att	720
Tyr	Asn	Leu	Ala	Asp	Phe	Val	Asn	Lys	Ile	Leu	Phe	Gly	Leu	Ile	Ile	
				225					230					235		
tgg	aat	ggt	gct	ggt	aaa	gaa	tct	tct	aat	gct						753
Trp	Asn	Val	Ala	Val	Lys	Glu	Ser	Ser	Asn	Ala						
				245					250							

<210> 63

<211> 251

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 63

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
1 5 10 15

Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
20 25 30

Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
35 40 45

Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
50 55 60

Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
65 70 75 80

Arg Gly Val Trp Ile Asp Thr Gly Asp Thr Pro Thr Val Phe Arg Tyr
85 90 95

Ile Asp Trp Leu Leu Thr Val Pro Leu Gln Met Val Glu Phe Tyr Leu
100 105 110

Ile Leu Ala Ala Cys Thr Ser Val Ala Ala Ser Leu Phe Lys Lys Leu
115 120 125

Leu Ala Gly Ser Leu Val Met Leu Gly Ala Gly Phe Ala Gly Glu Ala
130 135 140

Gly Leu Ala Pro Val Leu Pro Ala Phe Ile Ile Gly Met Ala Gly Trp
145 150 155 160

Leu Tyr Met Ile Tyr Glu Leu His Met Gly Glu Gly Lys Ala Ala Val
165 170 175

Ser Thr Ala Ser Pro Ala Val Asn Ser Ala Tyr Asn Ala Met Met Lys
180 185 190

Ile Ile Val Ile Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
195 200 205

Tyr Leu Met Ser Gly Asp Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
210 215 220

Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
225 230 235 240

Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
245 250

<210> 64

<211> 753

<212> DNA

<213> Naturally occurring gamma proteobacterium

<220>

<221> CDS

<222> (1)..(753)

<223> Proteorhodopsin variant from pcr clone PalE7; GenBank# AF350003

<400> 64

atg ggt aaa tta tta ctg ata tta ggt agt gct att gca ctt cca tca

48

Met	Gly	Lys	Leu	Leu	Leu	Ile	Leu	Gly	Ser	Ala	Ile	Ala	Leu	Pro	Ser	
1				5					10					15		
ttt	gct	gct	gct	ggt	ggc	gat	cta	gat	ata	agt	gat	act	gtt	ggt	ggt	96
Phe	Ala	Ala	Ala	Gly	Gly	Asp	Leu	Asp	Ile	Ser	Asp	Thr	Val	Gly	Val	
			20					25					30			
tca	ttc	tgg	ctg	ggt	aca	gct	ggt	atg	tta	gcg	gca	act	gtg	ttc	ttt	144
Ser	Phe	Trp	Leu	Val	Thr	Ala	Gly	Met	Leu	Ala	Ala	Thr	Val	Phe	Phe	
		35					40					45				
ttt	gta	gaa	aga	gac	caa	gtc	agc	gct	aag	tgg	aaa	act	tca	ctt	act	192
Phe	Val	Glu	Arg	Asp	Gln	Val	Ser	Ala	Lys	Trp	Lys	Thr	Ser	Leu	Thr	
	50					55					60					
gta	tct	ggt	tta	att	act	ggt	ata	gct	ttt	tgg	cat	tat	ctc	tat	atg	240
Val	Ser	Gly	Leu	Ile	Thr	Gly	Ile	Ala	Phe	Trp	His	Tyr	Leu	Tyr	Met	
65					70					75					80	
aga	ggt	ggt	tgg	ata	gat	act	ggt	gat	acc	cca	aca	gta	ttc	aga	tat	288
Arg	Gly	Val	Trp	Ile	Asp	Thr	Gly	Asp	Thr	Pro	Thr	Val	Phe	Arg	Tyr	
				85					90					95		
att	gat	tgg	tta	tta	act	ggt	cca	tta	caa	atg	ggt	gag	ttc	tat	cta	336
Ile	Asp	Trp	Leu	Leu	Thr	Val	Pro	Leu	Gln	Met	Val	Glu	Phe	Tyr	Leu	
			100					105					110			
att	ctt	gct	gct	tgt	aca	agt	ggt	gct	gct	tca	tta	ttt	aag	aag	ctt	384
Ile	Leu	Ala	Ala	Cys	Thr	Ser	Val	Ala	Ala	Ser	Leu	Phe	Lys	Lys	Leu	
		115					120					125				
cta	gct	ggt	tca	tta	gta	atg	tta	ggt	gct	gga	ttt	gca	ggc	gaa	gct	432
Leu	Ala	Gly	Ser	Leu	Val	Met	Leu	Gly	Ala	Gly	Phe	Ala	Gly	Glu	Ala	
	130					135					140					
gga	tta	gct	cct	gta	tta	cct	gct	ttc	att	att	ggt	atg	gct	gga	tgg	480
Gly	Leu	Ala	Pro	Val	Leu	Pro	Ala	Phe	Ile	Ile	Gly	Met	Ala	Gly	Trp	
145					150					155					160	
cta	tac	atg	att	tat	gag	cta	tat	atg	ggt	gaa	ggt	aag	gct	gct	gta	528
Leu	Tyr	Met	Ile	Tyr	Glu	Leu	Tyr	Met	Gly	Glu	Gly	Lys	Ala	Ala	Val	
				165					170					175		
agt	act	gca	agt	cct	gct	ggt	aac	tct	gca	tac	aac	gca	atg	atg	atg	576
Ser	Thr	Ala	Ser	Pro	Ala	Val	Asn	Ser	Ala	Tyr	Asn	Ala	Met	Met	Met	
			180					185					190			
att	att	ggt	ggt	gga	tgg	gca	att	tat	cct	gct	gga	tat	gct	gct	ggt	624

Ile Ile Val Val Gly Trp Ala Ile Tyr Pro Ala Gly Tyr Ala Ala Gly
 195 200 205

tac cta atg ggt ggc gaa ggc gta tac gct tca aac tta aac ctt ata 672
 Tyr Leu Met Gly Gly Glu Gly Val Tyr Ala Ser Asn Leu Asn Leu Ile
 210 215 220

tat aac ctt gct gac ttt gtt aac aag att cta ttt ggt ttg atc att 720
 Tyr Asn Leu Ala Asp Phe Val Asn Lys Ile Leu Phe Gly Leu Ile Ile
 225 230 235 240

tgg aat gtt gct gtt aaa gaa tct tct aat gct 753
 Trp Asn Val Ala Val Lys Glu Ser Ser Asn Ala
 245 250

<210> 65

<211> 251

<212> PRT

<213> Naturally occurring gamma proteobacterium

<400> 65

Met Gly Lys Leu Leu Leu Ile Leu Gly Ser Ala Ile Ala Leu Pro Ser
 1 5 10 15

Phe Ala Ala Ala Gly Gly Asp Leu Asp Ile Ser Asp Thr Val Gly Val
 20 25 30

Ser Phe Trp Leu Val Thr Ala Gly Met Leu Ala Ala Thr Val Phe Phe
 35 40 45

Phe Val Glu Arg Asp Gln Val Ser Ala Lys Trp Lys Thr Ser Leu Thr
 50 55 60

Val Ser Gly Leu Ile Thr Gly Ile Ala Phe Trp His Tyr Leu Tyr Met
 65 70 75 80

